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SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27833	58201	A	28003	1913	2388	PIIHNTTAMKKA AKAEPFTTIV CTE*AILSQRTCSL*FTVINDICP GPRAH/VVQDIHGKLTGSAIA NRFQDAMAIPFLGTQGKRVP NGMAIPFPGNRNVIAGAFIPHR QHLGQIQLNPNVRQCSNLFAHLL AQRSEAFHMRRHHRIRDTVKK TILF
27834	58202	A	28004	1	1566	
27835	58203	A	28005	951	1217	
27836	58204	A	28006	1294	3108	
27837	58205	A	28007	1	1896	LFDWLVSQNELKANPAKGVSA PKAPRHLPKNIDVDDMNRLLDI DINDPLAVRDRAMLEV MYGAG LRLSELVGLDIKHLDES GEVW VMGKGSKERRLPGRNAVAVI EHWL DLRDLFGSEDDALFLSKL GKRISARNVQKRFAEWGIKQG LNNHVHPHKL RHSFATHMLES SGDLRARGAYLC AKLLSGAAQ VPEWRSFAFWARCAEQARQN QYLQVSSCVPALEGCDVNGAS FTLEQMLAWRDHPQVTGLAEM MDYPGVISGQNALLDKLDAFR HLTLDGHCPGLGGKELNAYITA GIENCHESYQLEEGRRKLQ LGM SLMIREGSAARNLNALAPLINEF NSPQCMLCTDDRN PWEIGHEG HIDALIRRLIEQHN VPLHVAYR VASWSTARHFGLNHLGLLAPG KQADIVLLSDARKVTVQQVLV KG\EPIDAQTLPAEEIGRLAQFA PAYGNTIGRQPLSASDFALQFTP GKRYRVIDVIHNELITHSHSSVY SENGFDRDDVSFI AVLERYGQR LAPACGLLGSGSLNEGALAAT VSHDSHNIVVIGRSAEEMALAV NQVIQDGGGLCVVRNGQVTSE GAKERM MGKRYKETSGSIGLK VPAPLN LNLSLQPREQLGGQST
27838	58206	A	28008	1	3257	
27839	58207	A	28009	1	2145	
27840	58208	C	28010	193	363	
27841	58209	A	28011	1	397	
27842	58210	A	28012	2	405	FVSAQGPGGKRFGTAPATPGCL VHDLS*APCLR WYQHPT EEELR ILAGKQQKGKTKKDRKYNHI ESKPLTIPKDIDLHLET KSVTEV DTLALHYFPEYQWLVDFTVAA TVVYLVTEVYYNFMKPTQEMN ISLV

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27843	58211	A	28013	3	353	GYIEKRISCIALLF/SF*IPVNFLR FHDTFI*FCYSS*SIQLSLWQSQI LLCV*LLRSIDFLYLIW*PLTYN EHASILLSLRAPYQLFDL*NDRS HIRYSATLVNPNPVCFAVGHD
27844	58212	A	28014	106	1814	
27845	58213	A	28015	37	2847	
27846	58214	A	28016	1	2430	
27847	58215	A	28017	1	2660	
27848	58216	C	28018	80	328	
27849	58217	B	28019	1	1074	
27850	58218	A	28020	602	853	
27851	58219	A	28021	505	649	
27852	58220	A	28022	672	1903	
27853	58221	A	28023	3	319	
27854	58222	A	28024	1	219	
27855	58223	A	28025	2	508	
27856	58224	A	28026	1	1011	
27857	58225	A	28027	1	699	
27858	58226	A	28028	175	351	
27859	58227	A	28029	1	324	
27860	58228	A	28030	244	1335	
27861	58229	C	28031	115	231	
27862	58230	A	28032	2	139	
27863	58231	A	28033	1	788	
27864	58232	A	28034	115	358	LIVVRSRRGTSRSGSPRATAMA FKDTGKTPVEPEVAIHRIRITLT SRNVKSLEKVCADLIRGAKEKN LKVKGPVRMPTKVK*IVVRSRR GTSRSGSPRATAMAFKDTGKTP VEPEVAIHRIRITLTSRNVKSLE KVCADLIRGAKEKNLKVKGPV RMPTKVK
27865	58233	C	28035	179	283	
27866	58234	A	28036	57	431	
27867	58235	A	28037	54	440	RVPELWVGTEVKERKNARSGV PSTQRLECGSAESAAGAPASVS VQVTAVPAPLPFGWTGGGRAV NLTEAERMVVINSVCHWRLY E*TANRFS*KQDVGKLTNCVCH PEGMLKAVTTQAQVFLVIRHN
27868	58236	A	28038	1	2693	
27869	58237	B	28039	131	350	



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27870	58238	A	28040	1	594	MLDITNDQGNASQNHNAIPPYS CKNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTP LHPPALLAVDRGSRSSVPATDS LPSAHDRQQQFHTWVCSRLLA TVRADPADGQQPQARADVCGC RGTGFINLVMIHLMGFVGRIG QLEQVAPRPQGVSWVDSSDH LQGSPRVEPPGTWDLRVLCSQG Q*EAVNCGPQTPGLD/SFDYGH SCRSKVVSHCGFDLHFPDH**C KNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTPL HPPALLAVDRGSRSSVPATDSL PSAHDRQQQFHTWVCSRLLAT VRADPADGQQPQARADVCGCR GTGFINLVMIHLMGFVGRIG LEQVAPRPQGVSWVDSSDHL QGSPRVEPPGTWDLRVLCSQG
27871	58239	A	28041	1	285	
27872	58240	A	28042	1	1059	HNLSSSNSFPKMSFPNSSPAANT FLVDSLISACRSDSFYSSSASMY MPPPSADMGTYGMQTCGLLPS LAKREVNHQNMGMNVHPYIPQ VDSWTDPNRSCRIEQPVTQQVP TCSFTTNIKEESNCCMYSDKRN KLISAEVPSYQRLVPESCPVENP EVPVPRYFRLSQTYATGKTQEY NNSPEGSSTVMLQLNPRGAACP QLSAAQLQMEKKMNEPVSGQE PTKVSQVESPEAKGGLPEERSC LAEVSVSSPEVQEKESKEEIKSD TPTSNWLTAKSGRKKRCPYTK HQTLELEKEFLFNMYLTRER/R ALEISKSVNLTD\RQVKI\WFQN RRMKLKKMSRENRIRELTANL
27873	58241	A	28043	358	2292	
27874	58242	A	28044	2	300	HSL/SFFFFFFFFFFFFFFFFFFFF FFFLFFFFFFLLLLFVSFSFSFS SFSFSFSFSFSFSFFFFLLPSSSSS SSSFFFFFFFFLLLPFFFFFFMEH
27875	58243	A	28045	2	241	
27876	58244	A	28046	1	126	
27877	58245	A	28047	49	183	
27878	58246	A	28048	3	212	

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27879	58247	A	28049	13	494	WVVPKNKTTFCSEF/CGAFLWP NNNNNNFFFFFFFFFFFFFFFF FLLLPLLLPLLLLLPLLP SSSFFLLLSSSHSSPSSPSSPS SPSSPSSPSSSSSSSSSSSSSS SSSSSSSSSSSFSSFSFSFSFSF SFFFFFFFFLFED
27880	58248	A	28050	544	729	
27881	58249	A	28051	1667	1896	
27882	58250	A	28052	1	477	
27883	58251	A	28053	25	448	RSQFFFFFFFFFFFFFFFFFFFF/ ILLVLLLVLLVLLLLLLLLLLLL LLLL/ASSSSSPSPSPSSSSSS FSSSSSSSSSLGAYVLYFMVT HSPVLCCLCNLIINNI*EE*FFR FRHNCDFLAASTLGVDWLL
27884	58252	A	28054	47	376	
27885	58253	A	28055	1	1740	
27886	58254	A	28056	3	1464	
27887	58255	A	28057	1	394	
27888	58256	A	28058	143	429	STLQKKEARARHLVTPLDILQL FNGFPLLVDCKLLRYSRVHSF PRFWIFFSIKDHIGFPKENTQRK MRLHPPQSQ*TPPRE*VPSFSSG VGKSS
27889	58257	A	28059	165	408	
27890	58258	B	28060	21	253	
27891	58259	A	28061	1	150	
27892	58260	A	28062	1081	1303	
27893	58261	A	28063	147	437	

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27894	58262	A	28064	107	2499	PIEDPEGRRRMREFILRSIQGVL RMAPQIQPKPLLTKSSTSVSQA RL/TSKQKALLPRQCSGSAKAQ AEREKIEETCQVGMKPPVPGGY TLQGWITTFCNQVQLDTIKIN GCLKGKLIYLLGDSTLRQWIYY FPKVVKTLKFFDLHETGIFKKH LLLDAERHTQIQWKKHSYPFVT FQLYSLIDHDYIPREIDRLSGDK NTAIVITFGQHFRFPIDIFIRRAI GVQKAIERLFLRSPATKASVSK LKCFWEPTRTGTQKYEASQVTG AFPLRPKKGAATPSQLVIVNSS DAHNCDEESEVRIKSTLGLKL DCKKGTTALTKGTKEDEEDGAM SGVDQLCLLSSVDSSGRPQLMT DWHGVKGQFSCFKCGEEKELQ QKRKLTGKGWNVFFMVLEVG KTKIKALEVLASGKGTSWFIQ DFLAVNSSHGRWGKKEEFLFQ KWKVDPWLPVRWELVQTGT THLVPEGRSDSVTCAWMPLGS KQVYKEPAGFPDMLRLRGSRV RMAVVTVHSQRLNLSLGDQHF NYPLPLKKKKKKKKKDTLIYPA DWLESCQSDNLSLAERDLVLV LRLALCALYGLLAPGNGNTESA ELHPGDKTEAQRPMALFKVTR PLNERPGDLASHVSRFAKSFLK PAMESLECPQSRLVGEARKGHS ELVEKIERGCESTVGEGETTRKG SKRDHLDSQCKLGQRSQPWQG
27895	58263	A	28065	1	1770	
27896	58264	A	28066	85	204	SPCSTSPFRQLA**RRGPHRSPFP TVAHLIGEWRLMRNAG
27897	58265	A	28067	1280	1531	
27898	58266	A	28068	1	882	
27899	58267	B	28069	77	1188	
27900	58268	A	28070	1016	1400	
27901	58269	A	28071	1091	1770	CRGGSGCAVCAELAPGAVHTV AAERAGAQEAAAGAGPPQLGG LIAWATHLQHSAAVPLLSQRM CHTCCLSPRKLVLIGCRAAKSLSS SPCGKWLCAALIRQPSVKGLPS CGVPLPLSLSRIQMCSSEATSSW ELNPDFGEAATSP**ESGF/LQS VVSTALLPDNTTGETFHHDGRA DIGSQFIHRFLVCCHLLVLRWLI TLDTKADVVDIGHRLRCFDCRC VDSTICD
27902	58270	A	28072	1568	1819	

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27903	58271	A	28073	778	879	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY
27904	58272	A	28074	332	544	CMRRPSCSCPASIRDNTAPHSRT LKVLIIIGKLSSGRKLSRILPLLRS SSM*PTRAPN*SSASFTFTSVSG
27905	58273	A	28075	355	614	CMRRPSCSCPASTRDNTAPHSR TLKVLIIIGKRSSGRKLSRILPLLRS SSSM*PTRAPN*SSASFTFTSVSP L*NFIRLHPVY
27906	58274	A	28076	1	2226	
27907	58275	A	28077	31	117	
27908	58276	A	28078	1	547	
27909	58277	A	28079	290	730	
27910	58278	A	28080	3	267	TLVKVKDAEDQLGARVGYIEL DLNSGKILESFRPEERFPMSTF KVLLCGAVLSRIDAGQEQLGRR ITILRMTWLSTHQSQKSILRMA
27911	58279	A	28081	1	1785	
27912	58280	A	28082	551	685	
27913	58281	A	28083	2	211	
27914	58282	A	28084	1407	1874	PRAAAAPTNLSPELSASPRPRV ACASAWGAGTDVTGWAAAMP RVGRCLPRTGLGSARRLRPEL GGGAGPAPEAMRGFGADAGST EQPRLPARS*PRLPQRRPRKS ERPAGLAPRLRPPQPAEPPGLGS QERGRGTDRAAADPGLPRTSPE SS
27915	58283	A	28085	1284	1786	
27916	58284	A	28086	1205	1279	LALIVGNRS*MKPYQTTSVTPR CL
27917	58285	A	28087	423	676	
27918	58286	A	28088	2266	2367	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY
27919	58287	B	28089	743	852	
27920	58288	A	28090	1	1100	
27921	58289	A	28091	548	652	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY

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27922	58290	A	28092	1	2438	MRLFGYARVSTSQQSLDIQVRA LKDAGVKANRIFTDKASGSSSD RKGLDLLRMKVEEGDVILVKK LDRLGRDTADMIQLIKEFDAQG VSIRFIDDGISTDGEMGKMVVTI LSAVAQAERQRILERTNEGRQE AMAKGVVFAENDKKMLSNAFI ETADFRTLIEDDRTIVVGRRG GSFNLARAATRLWRYAMLME IASYISSHYKLSSQISSETLLNEH LKKWNSAQGDILRKRLVAKE YLDENNPEESIGDLQFNLNISEI ENNIVSLLERSDRKVILMDKL DEAYEPDNIGIGIAGLAYASIE LNQKAKCIRPIIFLRDNIFRSLSK EDPDYSRNIEGQVIRLHWDWA QLLMLSAKRMKVAFKLDIEKD QRVWDRCTADDP*KGGNGFKR CLQFTLYRPRDLLSLLNEAFFSA FRENRETIINTDLEYAAKSISMA RLEDLWKEYQKIFPSIQVITSF RSIEPELTVYTCLKKIEASFELIE ENGDPKITSEIQLLKASGILQSL YSVG FVGIRDKNTSSYSFCHDG RTPDKGFESNEKLLIHPCYWLG LNLNRNALAPEEAEIINDEYDI NIISDNSAIRNKTIGQITTHLDQI PIGNEGATEFEQWCLDALRIVF ASHLTDIKSHPNGNAVQRRDII GTNGGKSDFWKRVL EDYKTRQ VVFDAKNFEELGPSEYRQLQSY LTGPYGKLGFIINRDESEVVRSK
27923	58291	A	28093	673	916	
27924	58292	B	28094	1	4725	
27925	58293	A	28095	959	1387	CMRRPSCSCPASIRDNTAPHSRT LKVLIIGKRSSGRKLSRILPLLS SSM*PTRAPN*SSASFTFTSVCIS RCMSAVMVMVAVLTIA CRFLKM TVSVGHICSLNFALQTSTTAMA VPAAATRASRAQPNGRHPWRI CWKTQKA
27926	58294	C	28096	997	1302	
27927	58295	A	28097	659	2534	
27928	58296	A	28098	174	294	
27929	58297	A	28099	31	379	
27930	58298	A	28100	3	518	
27931	58299	A	28101	1	3015	
27932	58300	A	28102	40	198	QAARTTG FYAHL LRHYKTPVG HS*Y*WKLHGENKSSAFVC*P TCRNPFIDCW
27933	58301	A	28103	390	1186	

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27934	58302	A	28104	2	1287	GRVGFASTAQSPRILRSEPVRTP PIPAFSPKTLRIMSLHQFLLEPI TCHAWNDRDRTRPVCLDYSLV VSFEIKK*IALSPNNHEVHIYKK NGSQWVKAHELKEHNGHITGI DWAPKSDRIVTCGADRDAYVW SQKDGWVKPTLVILRINRAATF VKWSPLENKFAVGSGARLISVC YFESENDWWVSKHIKKPIRSTV LSLDWHPNNVLLAAGSCDFKC RVFSAYIKEVDEKKASTPWGSK MPFGQLMSEFGG\SGTGG\WVH GVSFSASG\SRLLGWG SATDSTV SVCWMPSKSLQVSTLKTFLPL LSVSFVSENSVVAAGHDCCPM LFNYYDRGCLTFVSKLDIPKQSI QRNMSAMERFRNMDKRATTE DRNTALETLHQNSITQVSIYEV DKQDCRFCTTGIDGAMTIWD FKTLESSIQGLRIM
27935	58303	C	28105	198	362	
27936	58304	A	28106	1	915	
27937	58305	A	28107	403	519	
27938	58306	A	28108	88	237	
27939	58307	A	28109	527	1205	
27940	58308	A	28110	2	272	
27941	58309	A	28111	39	543	
27942	58310	A	28112	1	789	
27943	58311	A	28113	401	912	
27944	58312	B	28114	147	653	
27945	58313	A	28115	586	650	KIQCLCLWLLFLIIFLHAFQETIL ALRVLVNFNKRINSLGKNLAFN LFVYNKANSMP*RLLWKAPRS DK*IQ*SLRIQNQCTQISSTAVH STVTKLRIKSRTQPLLQQL
27946	58314	A	28116	1	1464	
27947	58315	A	28117	260	462	MLYLSGI*PKAE/TIGAKWTIDL KSGSGKVYQGPAGKAADTHIL SDEDFHGRWGSASLTLRRHSLV AG
27948	58316	C	28118	183	254	
27949	58317	A	28119	98	445	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSG ACYMCRKSGHWAECPQPGIPP KPRPICVGPB*KSDCSTHLAATP RAPGTPAQGSLTDSFPDLLGLA AED
27950	58318	A	28120	32	143	

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27951	58319	A	28121	39	346	QYISELQFLASTVRQTPATSPA HKNFQTPEPQQPGIPPEPPPGAC YKCWKS GHQA KECLQPGIPRK/ HASHLWQPLPEPPGT LAQGS LT DSFPDLLGLAAED
27952	58320	A	28122	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNQPK EHL TNFKSAA ED
27953	58321	C	28123	80	106	
27954	58322	A	28124	166	423	RPRSERLLWGTSPLS/CALTL*G DPPTTSGPQTNQLKEHL TNFKS GPHWKMDCPH PAATPRAPGT LAQGS LTDSFPDLLGSA AED
27955	58323	A	28125	1	354	
27956	58324	A	28126	1	702	
27957	58325	A	28127	317	427	
27958	58326	A	28128	467	640	SARKRFQLSP**NKITLLKPASS AISALAATPRAPGT LAQGS LTD SFPDFLSLAAED
27959	58327	B	28129	1	320	
27960	58328	A	28130	1	605	
27961	58329	A	28131	273	529	LGSGDLPGWGINPLSSCSLLREK DPLTISGPQTHQPK EHL TNFKSG PH*KSDCSTAPG\ATPRAPGT LA QGAL TDSFPDLLSLAAED
27962	58330	A	28132	459	601	DVDRHVRGSNFHHNEIRSLAAT PRAPGT LAQ/GLTDSFPDLLGLA AED
27963	58331	A	28133	112	331	LGLGDLPGWEINPLSSCSLLHEK DPPTTSGPQTDQPKKRL TNFKS ATPRAPGT LAQGS LTDSFPDLL GLAAED
27964	58332	A	28134	1	579	
27965	58333	A	28135	72	300	
27966	58334	A	28136	722	820	
27967	58335	A	28137	1	624	
27968	58336	A	28138	348	636	
27969	58337	A	28139	134	1131	
27970	58338	A	28140	1	1209	
27971	58339	A	28141	2	764	
27972	58340	A	28142	3	805	
27973	58341	B	28143	1	861	
27974	58342	A	28144	1	1599	
27975	58343	A	28145	119	593	
27976	58344	A	28146	1	573	

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27977	58345	A	28147	163	593	GFLEVQTPHPPNLDGPRRANRN TFLWTVCHVGIPDLPALPAPASFL GTQLTLKKASDGPRTEKVTQD LAQPFWTTGRQLRFVLHLSLQQ KDLSKCWRGAEVVLGPTRLFL* GYSEGVKENGTTGGVVK*AFSM CDSKWFNPCLTF
27978	58346	A	28148	159	405	PRLRVKYTQLCIL*S/CWRERKK FHLGKRVELRQGTTLGRVGP KRRLSQGSAGCFPAGLAHSPPH LAEAPGSGFCTALFLWL
27979	58347	B	28149	123	1561	
27980	58348	A	28150	1	1771	
27981	58349	A	28151	68	698	
27982	58350	A	28152	1	1260	
27983	58351	A	28153	57	302	
27984	58352	A	28154	1	245	
27985	58353	A	28155	5	422	
27986	58354	A	28156	3	1372	
27987	58355	A	28157	1	1653	
27988	58356	A	28158	586	867	
27989	58357	A	28159	1	1410	
27990	58358	A	28160	1	1441	MDIKKGITDISASLRVESGWEA RTRKEKTHINTVIIGHVDSGKST TTGHLIYKCGGVDKRTIEKFEK EAAEMGKCSFKYAWVLCLK AEREHGITIDISLWKFETSKYY VTIIGAPGHRDFIKNMITGTSQ A\D\CAVLIVAAGVGEFESWYSP RNGQTREHALL\AYTLGC*NKL IVGV\NKMDS\T\EPYPYS\QKRYE EIVKEGSTYIKK\IGYNPSTVAF VP\ISGW\NG*QHCLEAKWLTCP WFQGDGKVTP*GLAIASWEPR LWRALALQSYPPTRPTDQAPLR PASPRMSYQKLGGIVNVATEV KSVEMHHEALSEVLPGDN/VGA FNVKNVSVKDVRRGNVAGDSK NDPPMEAAGFTAQVILNHPGQ ISAGYAPVLDCHTAHIACKFAE LKEKIDRRSGKKLEDGPKFLKS GDAAIVDMVPGKPMCVESFSD YPPLGRFAVRDMRQT\VAVGVI K\AVDKK\AAGAGKVTK\SAQK
27991	58359	A	28161	125	370	
27992	58360	A	28162	156	547	
27993	58361	A	28163	108	919	



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27994	58362	A	28164	1	712	LNSEGNSSGSGDSISYDAPAGNS FLEDCELSRQIGAQLKLLPMND QIRELQTIIRDKTASRGDFMFSA DRLITLVVEEGLNQLPYKECMV TTPTGYKYEGVKFEKGNCVSI MRSGEAMEQGLRDCCRSIRIGK ILIQSGGETHRAQVYYAQFPPDI YRRKVLLMYPILQTG\NTEFEA VKVL*DHGVHPSVIIQLSPFLIP HGGQ\SIQRFPEFPI*PTEVHPV APTHFGQKYFGTD
27995	58363	A	28165	1	606	GIRSAMQNTQNLLQMPYGCGE QNMVLFAPNIYGLDE\NLETQQ LTPEIKSKAIGYLNTGYQRQLN YKHYDGSYSTFGERYGRNQGN TWLTAFLVLTFAQARAYIFIDE AHITQALIWLSQRQKDNCGFRS SGSLLNNAIKVNHSGASFDLSI MISARMRIGSDNVKNSKGKPQ RKIKPGWHQKRGDRTKVDCDT LSYRDGYG
27996	58364	A	28166	1	4626	
27997	58365	A	28167	15	4479	
27998	58366	A	28168	256	852	
27999	58367	A	28169	319	405	
28000	58368	A	28170	606	896	
28001	58369	A	28171	1	372	FRRVACVGSAGD\TAGAEP/RG ACATAWVCEMAADISESSGAD CKGDPRNSAKLDADYPLRVLY CGEYCEYMPDVAKCRQWLEK NFPNEFAKLTVENSPKQEAGISE GQGTAGEEEEEKKKQKRGT
28002	58370	A	28172	1	731	LSRGSAAAGGRALGRPWGARRV ACVGSAGD\TAGAEP/RGACAT AWVCEMAADISESSGADCKGD PRNSAKLDADYPLRVLYCGVC SLPTEYCEYMPDVAKCRQWLE KNFPNEFAKLTVENSPKQEAGI SEGQGTAGEEEEEKKKQKRGR GQIKQKKKTVPQKVTIKIPRA KKKYVTRVCGLATFEIDLKEAQ RFFAQKFSCGASVTGEDEIIHQ DFTDAI\DVIEKWPEVG**QPL EDLGRK
28003	58371	A	28173	335	2297	
28004	58372	A	28174	23	416	
28005	58373	A	28175	1	681	
28006	58374	A	28176	1	1668	
28007	58375	A	28177	1	1587	

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28008	58376	A	28178	250	687	AATSLPFRASSTIASANSILRVGV MTSIHHFVFSKRVCNFTSKTY FMSQQSSRTCTDGGYQALPFSC SSVSPSQQTQIKSVRPDYLI.I.VE PPHHMGPSFFASSGLHYDQ*PH HRLHLYWVFSARPWNGDLNPS SAHDI*HE*PLHF
28009	58377	C	28179	45	179	
28010	58378	A	28180	743	1478	
28011	58379	C	28181	151	351	
28012	58380	A	28182	2	355	
28013	58381	A	28183	19	428	
28014	58382	B	28184	61	2118	
28015	58383	A	28185	1	1824	
28016	58384	A	28186	150	1552	KNMETEQPEETFPNTETNGEFG KRPAEDMEEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSPDSSGP ERILSISADIETIGEILKKIIP'LEE GLQLPSPTATSQPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQT'I KLFQECCPHSTDRVVIGGKPD RFVVECIKILDLISESPIKGRAQP YDPNFGWKPMFYG/GFTMMF DDRRGRPVGFPMRGRGGFDRM PPGRGGRPMPPSRDYDDMS'P RGPPPPPPGRGGRSGSRARNLPL PPPPPPRGDLMAYDRRGRPGD RYDGMVGFSADETWDSAI'DTW SPSEWQMA YEPQGGSGYDYSY AGGRGSYGD LGGP IIT'QVTIPK DLAGSIIGKGGQRIKQIRHESGA SIKIDEPLEGSERIIITGTQDQI QNAQYLLQNSVKQYSGKFF

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28017	58385	A	28187	221	1634	KNMETEQPEETFPNTEINGEFG KRPAEDMEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSVDPSSGP ERILSISADIETIGEILKKIIPTEE GLQLPSPTATSQPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD RVVECIKILDLISESPIKGRAQP YDPNFYDETYDYGGFTMMFDD RRGRPVGFPMRGRGGFDRMPP GRGGRPMPPSRDYDDMSPRR GPPPPPPGRGG\RGGSARNLPL PPPPPPRGGDLMA YDRRGRPGD RYDGMVGFSADETWDSAIDTW SP\SEWQMA YEPQGG\SG\YDYS Y/AQGGRGSYGDLGGPIITTQVT IPKDLA G/SLFIGKGGQRIKQIR HESGS/SSIKIDEPL\EGSEDRIITI TG\TQDQIQ\NAQYLLQ\NSVKQ
28018	58386	A	28188	218	497	
28019	58387	C	28189	183	254	
28020	58388	A	28190	1	1056	
28021	58389	A	28191	825	933	
28022	58390	A	28192	1	201	LVGHDRQGEHVCFYENYAEIG NR*GRNLGLTEVTGAVCEALR QYSPGNLLSLMGVRVSPSESEE
28023	58391	A	28193	450	509	
28024	58392	A	28194	2	71	SLTIPQPLSPFNLGVTLQSLPSLN FSSFPLVENGDAFYLAATLRA PGTVAQGS LTPSQIFSA*WRHPS ISPFS
28025	58393	A	28195	213	350	AVSHLCGTPLEIRLFNSPGSHSQ SPWNSGPRLSD*LLPRSSGLSG
28026	58394	A	28196	372	782	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQTDQPKHLTNFKSE KKETRFIRGPKTPAPVMD*GRQ PSLGV*PLQGCLSDYSPRFQRC QTTQGHLPWSFTLSSKSHFSGG RGKSLQVPEIWPPGQGMPAA QDSS
28027	58395	A	28197	189	380	SLCIFSSASALQQWQHEGWC GQLLPRGHGPNRKLQQQRQWI LL*VPEILPLGQGMPAAQDSS
28028	58396	A	28198	33	302	FRICALSTKLFCLSTPWCQTHIL SYPQYLP LPIYSVLDLRHAFFT IALHPSSQPLFAFT*TDPDTH*A QQITWAALPQGFTDSPHYVQ

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28029	58397	A	28199	1	532	MRVRNREEGNVVGKWGERQVD QRDAVMRVRRCGIWNNVGDRIE VRAENNGNCGTQQRVGTTGA GGAESISVRLPRRSGSVSLQLLS REDLGRSQESLGPEFQGLWK WLPDESSVWPAPGCLLLYCTH VDKEKGRRSLHVEHA*QLKTD AARSPRKPDYTFCSPGSFSCTH S/SVESHNYHCSRPGQLQSGLPHY SRYHT*PS*LH\SLIHLTFTPFPHI SFFPVSHPH
28030	58398	A	28200	266	397	SVHCQRFCRNRPVPLVENQILTG ETNILHTCMHTWF*DHVWKVT
28031	58399	A	28201	21	549	LGPLPFSLSPCCLHCQGKRLCG HHEEARRRKNVSIPRKEAGIIHC KGHQK\ASDPIAQDNAYADKL AKKAASVPTSVPHGISQAPPPLP THQARYWQIDFTHMPRVRKLK YLLVWVDFTGWVEAFPTGSK KATAVISSLLSDIIPQFSLPTSIHS DSRLAFISQITQAVSQALGIK
28032	58400	A	28202	3	518	KRPHPYLPLLTLFSDSAHLHPG EINNHVATRPPVWWSLHTDVH EIWCRDSDRGTSLSGRSIPCPVL CSVRKIHLQPQVLRPTSPRNISPI LNQVSGFLLLSSPTSLTPQPPLS PFNLGATLQS/APFS*FQFLSFSG RDKGDTFYPWSQNSGACHRLG KAAFPWCLIIAGTPL

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28033	58401	A	28203	3	1626	SEGEAKGSITLTVCTALYLKLT LFHKTGVFGPLRFPVNTLNPS PFHDGTRELGASEAIGQCQSSA AKLRRSGKESESLGPEFQGLWK WLPGSSQCFARESLEEKLSLCF RPSDPGAEPRTAVRPITERSLL QGDEYCCALGQGVNPWSTDR YWNWATLQEIGPSSCRKTSSGL PLILRYGHVRDLHGSSSHHRPG GPKRNKWFRELGLGSACCMRP RDLVPCVPAAPAVAERGESTA QAVASEGASPKPWQLPGGVGP VGAQKSRIEVWEPLIFRRMYG KACMSRQKFAAGAGFSWYVPV AVVGAKVHDVNLHMLSFPSPK WKLHTCMKFGAVTQIVTSLGR SSCSLLEKDPPMVLRPTSPRNI SPISNLTKETRFIRGPKTPAPVT DWEGLPLVFNHCRDASLIHP GFRGVRPRRDACLSPPLANLIN LTFKVYNNRKKLQFLAFTVRQ TSAMSPAHKNFQSLNLSGQAF LQNLLPQELATSARNPATRPRN ACSPGFLLSHVPSVRDPTGNWT VQLTWHPLPEPELELWPKAL
28034	58402	A	28204	921	1009	
28035	58403	A	28205	1	1005	
28036	58404	A	28206	1	2706	
28037	58405	A	28207	1336	1490	
28038	58406	A	28208	466	560	
28039	58407	A	28209	863	1672	
28040	58408	A	28210	1	876	
28041	58409	A	28211	133	746	SVKMVRYSLDPEN\PMKSCK/S QRGSNLRVPFKDHS*KLPQAHQ RVCHIRKSPTKY\LKDVHLTRN QCVPIPDYNG*QLGQVCRRPK QMGP GTTKGR\WPQKGVLKFL PAHALKTAEM*C*TLRVLDVDS LVIEHI\QVNKAP\KMRRRTYR AHGRINPYMSSPCHNIEM\ILTEK EQIVPKPEEEVAQKKKIS\QKKL KETPTLWHGE
28042	58410	A	28212	3	466	
28043	58411	A	28213	1	2772	
28044	58412	A	28214	1	1353	
28045	58413	A	28215	195	285	DIHLLYPVG/RNRGICRKK*RLR S*DY*CWR

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28046	58414	A	28216	23	561	CRPRKFYYEEDWLITKLKGQVS QESLSEKASSQATLPNQPVKEAI IMQLGTLLTFLHELVPTALPSGS CVDTL/SKGLVQNVHHTYSPCQ NFISRCVRAPEEFQKIWNSW*SC LVLI*PPCVILSFLYVQNKSKSL NYTGEKKEKPAAVATAMARVL RETKPIPNLIFAIEQYEKFLHPPV
28047	58415	A	28217	2383	2651	
28048	58416	A	28218	125	1396	
28049	58417	A	28219	466	643	
28050	58418	A	28220	73	150	
28051	58419	C	28221	1	240	
28052	58420	A	28222	2	499	
28053	58421	A	28223	192	351	
28054	58422	B	28224	1	2103	
28055	58423	A	28225	247	400	
28056	58424	A	28226	288	589	WCSRRRGWYLLLGFNHYWRSS TFLVRCTPSCPGGCCPRYGIYPV RSCPRLPGGVSRYGSIHSG/RWC SWSPSWSPWLTSVTPRLYVAL M*AVVCPVVGKQP
28057	58425	A	28227	319	398	
28058	58426	A	28228	1299	1506	
28059	58427	A	28229	1250	1907	
28060	58428	A	28230	547	638	EKRKSNCPCQLQMT*LYI*KTPSS QPKISLS

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28061	58429	A	28231	488	2358	RLSLGHWAAAGKQGASDSCEKP TQPPSGVLESTTP/CAAPSPPNR DSGPCPASSPGLSRPLLSGTAW APPPAPPWARVRPPREVWRAD LLTPQGGGPATGVSGGECDSP VGGNPGIWKA WGHRRTRVAGI GRRGGPGEADKQPLLVLRLQTG SGVDLQQTPDLQLRVLTVRR NTNKRKGHPHQNPICSPSSKT EGRSMRQKVNKDIQELNSALH QVDLIDIYRTLHPKSTEYTFSSA PHHTYSNIDHIVGSKALLNKCK RTEIVANCLSDHSAIKPELRIKK LTQNCSTTWKLNLLNDYWR SKRKTHSKASRRQEITKIRAEK ELETQNTLQKINESRSWFFENIN KIDRLLELRIKKEREKNQIDAIK NDKGDITTDPTKIQTITREYYKH LYKNKLLNLEEMDKFLDTYTL PRLNQEEIESLNRPIGYEIEAI NSLPTKKSPGSDGFTAIFYQRY KQELVTFLKLFQSTEKEGILPN SFHEASIIIPKPGRDTTKENFR PISLMNIDAKILNKILANQIQQHI KKLIHHDQLGFIPGMQGLFSTC KSINVIHHINKTKDKNHMIIISID AEMASDKIQPFMLKTLNKLGI DGMYLKIIRAIYDKPTANIILNG
28062	58430	B	28232	1	2664	
28063	58431	A	28233	767	969	KKRVFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPACPKRAPE GSTKHGKEQVPVATAKTGQIV
28064	58432	A	28234	804	920	RDIYSNKCPQEKPEKI*NGHPNI TIKRJREARAKTFKS
28065	58433	A	28235	786	935	
28066	58434	B	28236	3	1555	
28067	58435	A	28237	895	1389	GELLEVMTLAWSWGLFLARII QTQVFKAFLNLFVLIRSSWAF WTHGDELWALVSRKPK*HPGF CDHAPSTFPPPGGLCP/EPTPPGA VSQYPCPPSPCPWPRWLVLPLP VLAGTSSPWKGFSPYPPCCFSPF HLPARFLHRGNCLSTFDLVVLP PLEMPVLALS
28068	58436	A	28238	704	799	EKRKSNCLCLQMT*LCI*KTPSS QPKISLGW
28069	58437	C	28239	178	1287	
28070	58438	B	28240	1	1028	
28071	58439	A	28241	476	678	
28072	58440	B	28242	1	1059	
28073	58441	B	28243	1	924	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28074	58442	A	28244	39	200	LPLFLIECPLFSPA*LPWPGLPT LC*IGVVREGIPVLCPFSGMLP VFAHSV
28075	58443	A	28245	225	314	
28076	58444	A	28246	243	311	
28077	58445	A	28247	21	1593	RKRTAPAGPRRHPKHCECPNCG SGKGRPS/CSQTHPPPGKLKSSP *SRKAENSKNQSAFSPKDHSSS PVMEQSWMENDFDELTEVGFR SLAETQQQQKEKFRPISLMNID VKILNKILANRIQQHIKKLIHHD QVGFISGMQGWFNICKSINVIH HINRTNDKNHMIISIDA EKAFD KIQQPFMLKTLKKLGIDGTYLK IIRAIYDKSTASIILNGQKLEAFP LKDRTRQGCPLSPLLFNIALEVL ARAIQEKDIKCIQLGKEKVRL SLFAEDMIVYLENPIVSAPNLFK LISNFSKVSGYKINVQKSQVFL YINNRRQRESQIMNEFPFTIARRR IKYLG IQLTRDVKDLFKENYKP LLKEIKEDTNKWKNMPCSWIG RINIMKMAILAKVIYRFNAPIK LPMTFFTELEKTTLKFIWNQK
28078	58446	A	28248	129	239	FFLTMSMECSSICLCPPLFR*AV VCRSP*RGPSHPL
28079	58447	A	28249	3	254	GTAWAPPAPPWARVRPPEKC GAPTCSHPREEAPRLASPAGKN VTPVPWGETQGSGRLGVTGEPE LLGLGGAGALARLISSLCW
28080	58448	A	28250	80	517	GHFLGQQPRPQLHSPAPD\PPAP TPTDAEGLPQQQQLPQLEPQPE CQGPVEAEARQLKSCMKPVRR RPAEEELKTKNMDDNTFAMAE HPDVQESVGPLVAPTPLRPWPQ MTLQVCWSLLEFHSRPLPGY HQRLQNSKDCCLFLP
28081	58449	A	28251	1	670	
28082	58450	A	28252	1450	1650	QWISRQKLYKPEESGGQYSTFL KKRIFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPGLPYKSS
28083	58451	A	28253	1010	1294	QRFSWQKLYKPEESGGQYSTFL KKRIFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPGLPYKSAPE GSAKHGKEQPIPTTAKTCQIVK TIQA
28084	58452	A	28254	41	812	
28085	58453	B	28255	1	2957	
28086	58454	B	28256	650	3212	
28087	58455	A	28257	1	556	



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28088	58456	A	28258	378	566	KHSQGILLQVPEIWPLGQGMPA SRDSS*AVSHLCGTPLEIGWSNL PGSHSQSPWNSGPRLSD
28089	58457	A	28259	1	253	
28090	58458	A	28260	409	884	
28091	58459	A	28261	1	2256	
28092	58460	A	28262	118	302	
28093	58461	A	28263	558	659	
28094	58462	A	28264	1	400	
28095	58463	A	28265	308	433	
28096	58464	A	28266	1	711	
28097	58465	A	28267	559	657	
28098	58466	A	28268	1	400	
28099	58467	B	28269	232	498	
28100	58468	A	28270	1	2978	
28101	58469	B	28271	128	290	
28102	58470	A	28272	3	193	DVNIFIRYGLWCFLSPFGLL*QF WRLEVQYQDAADSMSSGGDPLS HS
28103	58471	B	28273	125	197	
28104	58472	A	28274	1	1776	
28105	58473	A	28275	19	223	GFPNRTALPKNGNKNNGGEASM VRGCLERAET*GCPNGMPQGE RLSRFGLRTETTGTVTFRHLCL QQR
28106	58474	A	28276	3	334	
28107	58475	A	28277	2	1698	
28108	58476	B	28278	1	1281	
28109	58477	A	28279	198	532	NSLFLLCCLCQALVSG*CWPHK MS*GGFPLFLTGTIVS/GRNGTS SSLYLW*NSAVNPSPGFLFLVS RLLTIASISEPVIGLFRDSTSSWF SLGRVYVSRNLSISSRFSSLFA
28110	58478	A	28280	3	610	TDFCFWFLPGLSVFLSFFLSF FLSFFLSFFLSLSFSFLSLFLS VLSFLPSFLFLSLSLSLFLS LL/YCLSFLSLSFFLFLSFLSS SLLFSSLLFSSLLFSSLLFLLLLL LSLSLLFFLSFLFSESVLWEGSV AGLQTPALSSALNRAVLVSCS MIDQLCDPGKYFISLCLFLHLR VRTCGVWFSVLVIVC
28111	58479	A	28281	203	470	QAKSVWKKILSFRI*LHRMSDG IFWLCFYISMHLWCWLVLWAV WFKLQTTRLSRWLTDPLVSY GYCQGMNEGCSSQFKTVFPTLF SAS
28112	58480	A	28282	164	338	GGGGVHVYQTS/GDIRKKEISK EISKG/LTKTPRLLVMSPSSCSR RGIWPNPDTCPLLLL
28113	58481	C	28283	1	603	

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28114	58482	A	28284	179	445	QLSGLASGMRESRDVLGLRFTP LLWIVHSRAWLVESAVMST WECWVGDERGTGVKLAGAHT ELPTGPGV*YSPPCVHVFSLFNS HL
28115	58483	A	28285	128	381	
28116	58484	A	28286	1	1392	
28117	58485	C	28287	1	3169	
28118	58486	A	28288	1905	2449	AQLPTAPLPFLGRRWGTWGFP GHAFHSWFWYSTGEGAMGSF LALLSFPLGMKLAILEDFFGIS GTAAPLGSSFGSSLRSSLSVTEA LLARSL/HFLILLPLLFLLFLIA FQRTLLVGQCPAKSPLGNALEC NLGAAGSRAHGGEHATGGLQL LALFEAGQSLQPLTACVPGPRP LTCL
28119	58487	A	28289	693	905	EESIS*KWPYCPSFHNLHPQAY KAIPHPASLGKT*YNQDNNNAG KLFKANRNPALGCQQPVCSKT DGFRF
28120	58488	A	28290	3	427	
28121	58489	A	28291	1	1195	
28122	58490	A	28292	158	779	
28123	58491	A	28293	227	378	
28124	58492	A	28294	1	621	
28125	58493	A	28295	1	351	
28126	58494	A	28296	1	507	
28127	58495	A	28297	1	543	
28128	58496	A	28298	343	428	
28129	58497	A	28299	785	1178	

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28130	58498	A	28300	842	2592	IREEVESLKRPIITSSDIEAVINSL SIKKKVQYQTDSQPNSTRGENL GNTIQDTGMGKDFITKTPKAM ATKAKIDKWDLIKLSFCTAKE TIIRVNRQPTWEKIFEIYPSNK GLISRIYKELKQIYKKKTNDPIK KWAKDMNRHFSKEDIYAACK H/DEKMLIITGTWMKLETIILSK LTQEQTCKHRMFSLIPDDGNS LTRRMLLIGISVKTPVGTGAIPG PVGTTAAGAYGRKEKALSNC DSILALALAKMSENQMSMESFF EKGKDPMRQKTLTLTKKKN AFKRKYQESYLNYGFIATVRAS FLVANCIVKAKKPFTIGEELILP AAKDICYELLGEAAVQKVPHV PLPVSTITRPIDEIAEDIEAQFLE RINESLWYTIQIDKSTIADNKAT MLVFVQYIFQEDVHEDVFFQES LRATSQPLKTPQTGKEWVHDPF VDKPSESTLSMLEEDQLEIAN DGLKSMFEKTSNLHIVCIKVK AEYPEIATKALRRLAAPPWVAA VDRECQWGSRDVEMRRLDPK AGFSLGVGNGCHCLRTLEFVGL SMSSLCGAMLLCGLRAAPYISL RDHKGQGTLL
28131	58499	A	28301	1	1662	
28132	58500	A	28302	2	406	CWWDCCLVQPLWKS VWRFLR DLELEIPFDPAI LLLGIYPKDYKS CCYKDICT/RVCVPAALFTIANT WNQPKCTSMIDWVKMWHIY TMEYY\AAIKKDEFMSFAGT*M KLETIILSKLTQEQTCKHRMFSL YWKS
28133	58501	A	28303	1	1404	
28134	58502	A	28304	68	2269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28135	58503	A	28305	189	1890	MKMASSLAFLLLNFHVSLLLV QLLTPCSAQFSVLGPGPILAM VGEDADLPCHLFPTMSAETME LKWVSSSLRQVVNVYADGKEV EDRQSAPYRGRTSILRDGITAG KAALRIHNVTASDSGKYLCYFQ DGDFYEKALVELKVAALGSNL HVEVKGYEDGGIHLECRSTGW YPQPQIQWSNAKGENIPAVEAP VVADGVGLYEVAASVIMRGGS GEGVSCIIRNSLLGLEKTASISIA DPFFRSAQPWIAALAGTLPILL LLAGASYFLWRQQKEITALSSEI ESEQEMKEMGYAATEREISLRE RKKIQYLTPDVILYPDMANAIL LVSEDQRSVQRAEPPHDLDPNP ERFEWRYCVLGCEFSMSERHY WEVEVGDRKEWHIGVCSKNVE RKKVWVKMTPENGYWTMGLT DGNKYRALTEPRTNLKLPEPPR KVGVILDYETGHISFYNATDGS HIYTFLHASSEPLYPVFRILTLE PTALTVCPIPK/GREFPRFPTLVP DHSLEIPLTPGLANESGEPQAEV TSLLLPAQPGAKGLTLHNSQSE PYSYRHTLKHFTDIHSIP

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28136	58504	A	28306	172	1905	MKMASSLAFLLLNFHVSLEFLVQ LLTPCSAQFSVLGSPGILAMV GEDADLPCHLFPTMSAETMELR WVSSSLRQVVNVYADGKEVED RQSAPYRGRSILRDGITAGKA ALRIHNVTASDSGKYLCYFQDG DFYEKALVELKVAALGSDLHIE VKGYEDGGIHLECRSTGWYPQ PQIKWSDTKGENIPAVEAPVVA DGVGLYAVAASVIMRGSSGGG VSCIIRNSLLGLEKTASISIADPF FRSAQPWIAALAGTLPISILLLA GASYFLWRQKKEKIALSRETER EREMKEMGYAATEQEISLREKL QEELKWRKIQYMARGEKSLAY HEWKMALFKPADVILDPDTAN AILLVSEDQRSVQRAEPRDLP DNPERFEWRYCVLGCENFTSGR HYWEVEVGDRKEWHIGVCSK NVERKKGWVKMTPENGYWTM GLTDGNKYRALTEPRTNLKLPE PPRKVGIFLDYETGEISFYNAID GSHIYTFPHASFSEPLYPVFRILT LEPTALTICIPKEVRRVPPI/AD LVPDHSLETPLDPGA*LMKVGE PQAGK*HLCFSLPTLGAEGLPF
28137	58505	A	28307	1	2220	
28138	58506	A	28308	134	509	
28139	58507	A	28309	80	433	VKTELVGWGPSRRGWGAQRSP AEKMGETPGA AVSRIRLGGRV ALRRHVRGEPLRAPDCPLGPDA WVPTRGSHFPGFFPREQSLS/W GATPPSYRSSEVRSGAESGRPA DSVGSQVQAH
28140	58508	A	28310	1	1066	
28141	58509	A	28311	77	273	
28142	58510	A	28312	1	415	
28143	58511	A	28313	11	257	
28144	58512	A	28314	1	654	
28145	58513	A	28315	2	671	PGEFTRAPVRRRAMGISRDN WHKRRKTGGIRKPYHKRRKYE LGRPAANTKIGPRIHTVRVRG GNKKIYRALRLDVGNFWSGSQ CCTRKTRIIDVVYNASNNELV TKTLVKNCIVLIDSTPYRQWYE SHYALPLGRKKGAKLTPEFEEI LNKKRSKKIQKKYDERKKNAK ISSLLEEQQQGKLLACIASRPG QCGRADGYVLEGKELEFYLRKI
28146	58514	A	28316	3	1259	
28147	58515	A	28317	1745	2681	

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28148	58516	A	28318	1	2502	
28149	58517	A	28319	1097	1417	
28150	58518	A	28320	1	398	MTAEERDKFPTDQQAIPSMDPH WDPDSHDGDSHKLHLLTCVLE GLRRIRKKPMNYSMMSTITQG KEENPSAFLKWLREALRKYTPL SPNSLRGQLILKDTFITQSAADI RRKLQKQALGPEQNLEALLNQ ATSVFYNRDQEEQAQKEKRLSS RSVTIRGILGQSVTRPEAHKGL QDIVKHLKAQGLVRKCSSDCN TPILGVQKLNGQWRLVQDLGLI NKAIIPLYPVVPNPYTLLSQISEE AEWFTVLDLKDAFFCIPLHSDS QFLFACEDPTDHTSQTQTILPH GFRDSPYLFGQALAQDLGHFSS SGTLALQYVDDLPLATSLEASC QQATLDLLNFLANQGYKASRS KAQLCLQQRDGGTTLYSNQGA PEGKYSSSRMRPRVRNSLQNLK AGPSTTPALSPLTGQNLSTLYVT ETAGIALGVLTQAHGMNPQPV AYLSKKIDVVAKGWPHCLRVV VAVAILVSEAIKIIQGKDLTVWT THDVNGILGAKGSLWSDNCL LRYQALLLEGVLQIPMCAALN PATFLPEDGEPIS**PLTLRWPLP QLPLNSEASLLLLHQFSYLGMP LVGGSSHEPA
28151	58519	A	28321	318	363	
28152	58520	A	28322	812	910	RAISCCPSHW*KEKPPWRPIRKP PLPARWPIH
28153	58521	A	28323	1638	2180	RSAASLLKSVRPRTHQEEETLD TSEHLKEQTADTSSLRTVTLTA RVCGFILEVSETKNSPEGTNSG HILTSQMGLSPIAKRRETSASAA ALVSATIPICRVQGPLRVLGQE VFLLLLRLPTAPLPINDKPP/PN/ TPLPRRKQAKKSPKDHKNPWAI GYVPFKQ*GEGNLA*PGYMSPS

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28154	58522	A	28324	350	1563	FLYIQLYPTPITCSLK YQRKQNG SLFWTSRMPSSVFPCTLTSPFSL PLRIP/PDHTSQLTWTVLPPGFR DSPPLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSSEASCQQA TLDLLNFLANQGYKVSRKAQ LCLQQVKYLGILAKGTRALIK ERIQPILAYPCPKTLKQLRGFLG ITGFCQLWIPGYSEIARPLYTLIK DTQRANTHLVEWESEAETAFK TLKQALVQAPGLSLPTGQNFSL YVTERAGIALGVLTQTRGTTTPQ PVAHLKETD VVAKGWPHCLR VVAAVAVLVSEAIKIIQKDLIV WTTHEVNGILGEKEVYGYQTN AYLDTRRSALRDWCFKYARPV AAILLLAFGPCIFNLPVKFVSS RIEAIKLQMVLMQMDPQISSTNN FYRGPLD
28155	58523	A	28325	830	1143	
28156	58524	A	28326	234	510	PWQSLP*VAQKVPKDHRSPLPE P*TRSLNNS*QHWLCPPARAP STCSTSCPARDGPPPPSPAPHGP RNTSVPGVHSRPGSPPPAPPRTTP VS
28157	58525	A	28327	2	816	
28158	58526	A	28328	1	1311	
28159	58527	A	28329	764	937	
28160	58528	A	28330	1	1389	
28161	58529	A	28331	1	484	
28162	58530	A	28332	72	299	
28163	58531	A	28333	737	847	
28164	58532	A	28334	1	2072	
28165	58533	A	28335	68	223	
28166	58534	A	28336	468	596	
28167	58535	A	28337	358	661	
28168	58536	A	28338	72	300	
28169	58537	A	28339	65	244	
28170	58538	A	28340	2	584	GKSRRMFPAQEEADRTVFVGN LEARVREEILYELFLQFLIAGPL TKVTICKDREGKPKSFGFVCFK HPESVSYAIALLINGIRLYGRPIN VQYRFGSSRSSEPANQSFESCV KINSHNYRNEEMVVGRSSFPM QYFPINNTSLPQEYFLFQKMQR HVYNPVLQLPYYEMTAPLPNS ASVSSSLNHVPDLEAGPSS

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28171	58539	A	28341	2	367	MTMHYEIPVTRRRSKGTT*LPO NA/SVNNMPH*TGAI*ADISM <sup>TN</sup> YARIERNHLGRGNSNSKDPKLR ESSEHLRKLKTRVVNEQTRI.GI. IMETFVGRGGEAPFYFQCDKHL SRSFQGLGLICL
28172	58540	A	28342	98	387	RKQPPKVLQWLLAF*SHRSW LSSPWPSDLWRPWAGGACARL LLQQPRDSASLKERQQPQSGAY R*NSHLPGTEHLGEGVAVCAAS ADLNV <sup>TAC</sup> WL
28173	58541	A	28344	1	269	
28174	58542	A	28345	240	483	
28175	58543	A	28346	3	1174	
28176	58544	A	28347	59	310	
28177	58545	A	28348	2423	3104	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC <sup>DVR</sup> VSILD <sup>SC</sup> FLL*AFSAIN <sup>FPLHTA</sup> LNASQRFWYVVS <sup>LFSLVSKNIFI</sup> SAFISLCTQ*SFRSRLFSFHV <sup>VER</sup> L*VRF/CNPEF*FDCTV <sup>V\WRDS</sup> LL*FLFFYIC*GELYFQ <sup>LCGQFW</sup> NRCGVVLKKMYILLIW <sup>GGFC</sup> RCLLGLLGAELSSIPGYSC
28178	58546	A	28349	2006	2830	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC <sup>DVR</sup> VSISDL <sup>SC</sup> FPLWAFSAIN <sup>FPLHT</sup> ALSASQRFWYVVS <sup>LFSLVSKNI</sup> FISAFISLCTQ*SFRSRLFSFHV <sup>V</sup> ERL*VRF/CNPEF*FDCTV <sup>V\WR</sup> *FV <sup>IISVLLHLLRRALLPTMWSI</sup> LE*VWCGAEKNVYSVD <sup>LGWR</sup> VL*MSIRSAWCRAEFNSW <sup>VSL</sup> TFCLVDLSFSLAALNIFS <sup>FISTLV</sup> NLTIMCLGVALLEEYLC <sup>GVLCI</sup>
28179	58547	B	28350	1	3135	
28180	58548	A	28351	3506	4187	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC <sup>DVR</sup> VSILD <sup>SC</sup> FLL*AFSAIN <sup>FPLHTA</sup> LNASQRFWYVVS <sup>LFSLVSKNIFI</sup> SAFISLCTQ*SFRSRLFSFHV <sup>VER</sup> L*VRF/CNPEF*FDCTV <sup>V\WRDS</sup> LL*FLFFYIC*GELYFQ <sup>VCGQFW</sup> NRCGVVLKKMYILLIW <sup>GGFC</sup> RCLLGLLGAELSSIPGYPC



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28181	58549	A	28352	2150	2831	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSLSLFSLVSKNIFI SAFISLCTQ*SFRSRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFPVCGQFW NRCGVVLKKMYILLIWGGGFC RCLLGLLGAELSSIPGYPC
28182	58550	A	28353	1	3531	
28183	58551	A	28354	1	3126	
28184	58552	A	28355	2357	3083	FFSLFFFILASGLSILLIPSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLLWAFSAINFPLHT ALNASQIFWYVVSLSLFSLVSKNIF ISAFISLCTQ*SFRSRLFSFHVVE RF*VRF/CNPEF*FDCTVV/WRD SLL*FLFFYIC*GELYFQVCGQF WNRCGVVLKKMYILLIWSGEF CRCLLGLLGAELSSIPGYPC*FF VLLICMLTVGC
28185	58553	A	28356	6412	7092	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLLWAFSAINFPLHT ALNVSQRFWYVVSLSLFSLVSKNI FISAFISLCTQ*TFRSRLFSFHVV ERL*VRF/CNPEF*FDCTVV/WR DSLL*FVFFYIC*GELYFQLCGQ FWNRCGVVLKKMYILLIWGGG FCRCLLGLLGAELSSIPGYPC
28186	58554	A	28357	1	2019	
28187	58555	A	28358	1	1263	
28188	58556	A	28359	77	304	
28189	58557	A	28360	1	756	
28190	58558	A	28361	1	369	QQRTLLASNEAFKSQAKSASQP ASKYMKENDQLKKGA AAVDGG KLDVGNAEVKLEENRSLKAD LQKLKDELASTKQKLEKAENQ VLAMRKQ/SPEGLTKEYDRILLE EHAKLQAAVDGPMDDKKEE
28191	58559	A	28362	879	1156	
28192	58560	A	28363	54	407	

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28193	58561	A	28364	620	1246	GSTWHGWDGSRCSQRWWS MTKRSSQPSSLS*SRRRRWMS SSPNW*KTGPSSMSRMSSAG* SAASSRSCATRWTRRRPAAWR G*GVTPVAWWPPWTCWSRPR EPGSGWPKPSVCWNSSEMRTT MSSSGSSTPWPVSRRRPWTER RLGVRGDRLRERSRPAVNRT RMSRVPSGAPRGTPSRRWWM MKCWDHQMRLVVEEVG
28194	58562	A	28365	86	402	KGWWCRKKGWNWKRWF FLQGLLEGPHPPSPTPAPRRTT* SLYSAPSRMVQVLLDDLHKWF LYSCLVSAISIGIKFPLKIHISPGS GVLEARETMSHFKEAAL
28195	58563	A	28366	54	353	
28196	58564	A	28367	66	352	
28197	58565	A	28368	442	700	HWNKVPAENPHLPWVRCSPT PLGKPKPCSSWNRRSGTDVSGT GLSESGSSWPSGSCNGVTGTDA YGP\GYVKSGSFPGPRVRGT
28198	58566	A	28369	1205	1722	WTDFRSIGLMALAGSVLELSAR SKDATPDPPRGLGKFPRLPQA PRLGSRLLSTLCSTLSGRGG KNTSRLSFSPSGSVKGRVRDV EPGPIRAHRTAFFPNASS\GSEG R*SPSVVAWRGFR/CVGVWRF TVGVWHAPPRCTR*SPITGSAP LSVWSPACTGSPTCTAGA
28199	58567	B	28370	163	387	
28200	58568	B	28371	112	419	
28201	58569	A	28372	1	1902	MSRIAWKLLWKLIQGYLGQPA GTARRHPGIGIFKSPPGDFTCNG LIAVIKNQSDNQRGMSPGSWSP GRENNPTLVEVLEGVVRLPETV HTAVRYTSIELVGEMSEVVDRN PQFLDPVLGYLMKGLCEKPLAS AAAKAIHNICSVCRDHMAQHF NGLLEIARSLDSFLLSPEAAVGL LKGTAIVLARLPDKITECLSEL CSVQVMALKKVFGATSRRVA KLFREGLKAHGNSFETSGEAER CCTWRPKEMTCVE
28202	58570	A	28373	1	2019	

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28203	58571	A	28374	2	1455	SAAVAARSPQPQRPSATLGPGP QRRPPSAAPTAWAAAAAPGS RRRRPLPARPLWAPARGAAAA GPAEAPMLARRKPVRAALTINP \\TIAEGPSP\\TSEGASEANLG\\DL QKKLEELE\\LDEQ\\QKKRLEAFL TQKA\\RRVGELKDDDFERISE\\ GAGNG\\GVVTKSPAQDPSGLIM \\ARKLIH\\LEIQAGASGNQIIPR/D LQVLHDGTWPTMGG\\FYGAFY SDGE\\ISICIEHMDGGS\\DQVLK E\\AKRIPEE\\LGK\\VSHRSFSGGL AYLREKHQIMHARDVKPS\\NILV \\NSRGEIKLCDFGVSGQLIDSM\\ ANSFVG\\TRCYM\\APERLQG\\TH YSVQSD\\WSMGLSLVELAVGR V\\PIPPRDAEELEAIFGRPVDG EEGEPHSISPRPRPPGRPVS GHG MDSRPAMAIFELLDYIVNEPP\\P KLPNGVFTPDFQE\\FVNKCLIKN P\\AERADLKMLTNHTFIKRSEG\\ EEVDFAGWLCKTPAG*TKPGTP \\TRTAV
28204	58572	A	28375	229	257	VLSASPLVSLAGRSPSRPLGRG CQSLDGYGVGWQAQSPGADE GNRSFT*PELADKNVPNLHVM KAMQSLKSRGYVKERLPSSAP GDCACHPTP
28205	58573	A	28376	3	397	MFNLRGKRLS/GNGRVFSLQAP KQK*PGGTEDS/YDASGPPPKF LIKEIKLGVPFFPIRGV*NP GPG KNFGGPFKKT*FCWARVPKM* FFKGGPSSSSPAVSLFNAKESSPI LLRWMTTSTTKSAYKLEFGC
28206	58574	A	28377	1	367	
28207	58575	A	28378	1	1001	MSWEMEQDEVYKEMSINHKN EGTRVEKPNRYRIIHIQPDAINH VSRKKDVPSASGAGHSRSSTGS RPGVRRLLWPLLLRSAPSGPLNN AVPAPGKGPGRWGGSPSLRSRG GKASTRVAPGLSAHSQAASGV PEPAEPQHQR TKASGSRRLSLR VVPEAPKPRTRTAREGKGAGA GHTGGAQEQRRLRRWACRGLR GRPGAVSPGGAEAINQLASEHC GNPAAALHRCIASLPRNLLVW AGRMLMPKKNRIAIYELLFKEE VTVVKKDVHMPKHLELADKNS RGYYVKEQFAWRHVYWYLTN ED/MPVSP*LPSSAPGDCACHPT PQPSRDWQASV

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28208	58576	A	28379	1	1827	
28209	58577	A	28380	520	680	AEACQSLDGYGVGWQAQSPG ADEGNHGDGTGYPHW*GTSRNV SRQTVQTRSLGT
28210	58578	A	28381	168	378	
28211	58579	A	28382	1	900	GTRDATAEENRVLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILPL FADKVPKTAENFRALST\GEKG FGL*GVPCFHRHPPGFMCQGGDF TRHNGT\GGKSI\YGEKFEDENFI LKHTG\PG\ILSMAKCWDPTQN GSQFFNLALAKTEWLGWASHV GVLAK*KKGMNIVEAMERFGS RNGKTSKMITTADCGQLRIKFD LVFYLNHQDHSFWKPQGEHPS NPFARRILRILWLSLAVPFVWVPC FPCSLPCLAGLQS
28212	58580	A	28383	393	683	HAKDGMERQGNNECPKVGKQ VTLQHS DPEDRKTSTRCGENLY MSSDPTSWSSAIQSWYDEILDF VYGVGPKSPNIVLLVII*IIERIPR TNKEHLVPV
28213	58581	A	28384	119	193	
28214	58582	A	28385	1	567	
28215	58583	A	28386	957	1145	EQNLLIYLVSI VQDCMDKGCII* LRHTSGN CMYVSDKFDFKEQCI FSPRSSQKSLSGNDLQK
28216	58584	A	28387	153	2257	
28217	58585	A	28388	369	539	KKPARRRHFLTLLCCVFSPKLC TAGGPMRRTFKSYDEAGTGLL SVADFRTVLRQYSINLSEEEFFH ILEYYDK\TLSSKISYNDFLRAFL Q*TPKL
28218	58586	A	28389	3	1364	
28219	58587	A	28390	1	996	
28220	58588	A	28391	296	549	ETSSSVTVSDP\EMENKGGQTL\ NNSSLMAEAPGTMC RFTLAPH V\LA VQGTITDLPDHLLSYDGSE NLSRFWYDFTLENSVLCDS
28221	58589	A	28392	1	1065	
28222	58590	A	28393	412	428	WILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW* KEKPPWRPIRKPLPARWPDSL MQLARQVSRLESGQ
28223	58591	A	28394	3	505	
28224	58592	A	28395	1	1201	
28225	58593	B	28396	518	1606	
28226	58594	A	28397	1	798	
28227	58595	A	28398	737	3067	

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28228	58596	B	28399	133	239	
28229	58597	A	28400	3	376	
28230	58598	A	28401	1	1194	
28231	58599	A	28402	405	611	
28232	58600	A	28403	204	4198	
28233	58601	A	28404	1	3346	
28234	58602	A	28405	824	1144	KSQSVQKITMFTFITQLLLVEV KDSLERLAVEVVFILQKAMYE KQAHYMKSLCPQMVLMLRFI QWVQIMPMLKLENLQHLMAR WNETVKEKK*DTLLFSMHERN
28235	58603	A	28406	359	517	
28236	58604	A	28407	68	487	
28237	58605	A	28408	2	154	
28238	58606	A	28409	3	297	RHKDSPPPHQTQEPSWLHPVDP APGLQVELPASHAPCARTPQPL GGRWDWAPWSRGWCSLGR LG PHRSPWSGWEAQA*QWIPHQG CRWSCLPVTRRVLALLSPWVV DGTGRRGAGGGARWGGSGRT GAHGVGGRLRHSRLQVPSPAL LFKYYYCDIFK
28239	58607	A	28410	1	609	MVFSNLKGHWLQPIRLDSGSR NTAIGCDNQYKPTGVKLQTF VSVTALKAAARLGLFVPPGGLV VSLGSGVKLQIFASQVVCFDRA LIGAFTIPELDTKVLHVPIRLVR YRVWTQRFKAPPDSGAQLASP SESHTRAAGGAACQSQCRA LLSPWVVDGTGRRGAGGGAHR GGSGCTGTHGVGGRLRHSG LPSSA*VSHPLRGFL/LQPEPPR* APPPAPRRPVPSTTQGLRSAGA RHWDWQAAPPAALVWDSLGE ASWAPESGGALENLCVHTLYL TNLMGTWRTFVSSSGIVNAPIS ALSKQTTWLAKICSFTPEPRETT SPPGGTNNPRRAALRAVTLTAK VCSFTPVGLYWLSQPMVAVLRE PESNLIGWSQWPFRLKKT
28240	58608	A	28411	548	753	TLLWE*SRLRKKSHLMMTLNH STHSITFGLDKHCASYLMGFLYI VELLIAQCSPGATLIQWRMAS MD

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28241	58609	A	28412	1	903	MAKKIQLTYKCVQNWWVLGL TDFKNEAADPRRVKLQTFVVS VTALKAAARLELFIPPGGFVVSL ASGVKLQTFAVSVTAHKGSD PKTRHKGSPSPHQTEPSWLHP VDPAPGLQVELPASPAPCARTP QPLGGQWDWVPWSRGRCSSG RLGPRSSPRWGAGSGMAGCRS RALPHGEAAKAQRKVTAAGP GAKHLTAWGWQGQLATPSVG PAEPHTQNSHWPASAVCSPSS RLRLSLHTYPQAEAGAGSGLGQP RKGLPQCSSLKGSSSAAKVGA QAEVPRASEACEG*RAPQVLP KWEPRQRRCRERARPARAAS LSPLISI
28242	58610	A	28413	1178	1480	CRHLIQSHSICLHQWDCHTOHL YHPQ**WNQQQQLHHRCLLQG SIHLVFGPQWDPRRRRPLRGTR SAMARMDILRISREYITQEITEA ATKRKVLSVPKE
28243	58611	A	28414	126	407	WIPHRGCRWSCLPVPICALALL SPWVVDGTGRRGAGGGARQG GWGSTGAHGVGRRLRHGGLQ VSPAPRESS*GPARNRSQRRRS DSSLRERK
28244	58612	A	28415	27	363	
28245	58613	A	28416	1	576	
28246	58614	A	28417	813	923	YSLIHAAPQQRS*SLSGPHQTY DISSYTCQCLKAVG
28247	58615	A	28418	511	1260	ARHRVLIGVFTIPELDIKVLHVP TRLRSPASFTQWIPHWGCRWSC LPVPRRVPALLSPWVVDGTGG CGAGGGAHRGGWGCTGAHGG GGRLRHGGLQVASPAPREGS*G PARN*AQSRWAGTAGGPSTPSA AAGPGAKPLIAPGRQGNEPCH WCGARQAHAPHELQLATSASW TRAFRECVSPAWPSCLGAACFH CLLIGPFPFSFSSQHLSTSLGHLV LLSWHLTSLSVSFRILTRLLRVF TGSWGGGAA
28248	58616	A	28419	1	616	
28249	58617	A	28420	2879	3022	
28250	58618	A	28421	3	165	
28251	58619	A	28422	340	793	
28252	58620	A	28423	912	3097	
28253	58621	A	28424	1300	1648	
28254	58622	A	28425	1	599	

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28255	58623	A	28426	2	405	PRVRPLRPPVMVSRDQAHLGPK YVGLWDFKSRTDEELSFRAGD VFHVARKEEQWWATLLDEA GGAVAQGYVPHNYLAERETVE SEPRDTQAVRHYKIWRRAAGR LHLNEAVSFLSLPELVNYHRAQ SLSHGLR
28256	58624	A	28427	3	438	
28257	58625	A	28428	37	403	
28258	58626	B	28429	1	1176	
28259	58627	A	28430	2	2150	
28260	58628	A	28431	1593	3025	
28261	58629	A	28432	322	2168	
28262	58630	A	28433	183	591	
28263	58631	A	28434	2	258	
28264	58632	C	28435	52	363	
28265	58633	A	28436	1	3363	
28266	58634	A	28437	1	918	
28267	58635	A	28438	1	1422	
28268	58636	A	28439	3	10899	
28269	58637	A	28440	277	586	
28270	58638	A	28441	3	3364	
28271	58639	A	28442	1	1851	
28272	58640	A	28444	3	253	CGIEDNNFSLALNPDTDILLS/HS GGRGAEAPTMCLKLTVSKRAC FEGLE\WQFNLWRNKK**C*DK KHKTAGCSIS*VMRSVYR
28273	58641	A	28445	1	950	MGSSAVQSQLAALAPRVLTGG LADVTALLRAPATPGRLVAGA RGGWGYVQSCRGAGAAAVKP LGSAETA VPIARLGCRRF SR SRC CRRRGRGSLLSFSAAKPIVFKEK LTMKTDLSMEEKLECSLWCCCL SDPSTPGRCCVLERRIVPWMQQ LLANIKQAEKHEKNHPEVTVA MALTDIDLQLQFSMSQPE/GPPS PGSRPS*PPPAALLWTPAGQA CPGPGGAEAADPSRNSTEWLRP PHHSSDCLRGLAHIVSQWVSEC LLCSPGSPRSPLWALCWEHWE TWPALPEGNQPSPEGLPPCSRS QWPQTTPASDPQ
28274	58642	A	28446	3	213	LTQHCWTHLVRSSHSRTGSSRL HNNQLHQPCA*S*LCQKEHASR GWSEQFNLWRNKK**C*DKKH KTAG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28275	58643	A	28447	142	772	LVNVDVDADLVGLCVSHRHTV EEQYSTLALLNHGPQVALKYV HMDEVPMMPACCLEGGCLPAL CGECKLQGSFILSAPGRQGSQR VGPREAQGHIVIGRKLSTALM LIGGQRLEESAIESGCMEATP QGMAGSPQVGQA KSPSPVNPKE PIGDF*GGSQDYRGGIQKPID*Q CGPVL/SRQSELWCGGRSHSVE FLLGSAASAPPGPGA
28276	58644	A	28448	1	1935	
28277	58645	A	28449	2	1571	
28278	58646	A	28450	2	301	PRPFYSKNFYKILSLYSSEFNNS FVDA\LGSD\QDSGNEDVFDME YTEAEAEELKRNAEVIVFIPEYS WSNSVSLFPLCPGAKGPTFSVH CRVHFGPFSSH
28279	58647	A	28451	1	1329	
28280	58648	A	28452	240	503	
28281	58649	A	28453	1039	1896	
28282	58650	A	28454	1	2397	
28283	58651	A	28455	1	4011	
28284	58652	A	28456	3	1088	
28285	58653	A	28457	1	4878	
28286	58654	A	28458	1	174	
28287	58655	A	28459	3	161	
28288	58656	A	28460	992	1102	
28289	58657	A	28461	1024	1279	CGHLVSDWSTVVNLAVRRLFV GFPQGCQLVHIW*M/PLDAGPE HNSLKGFLVPLFPLAATPRAPG TPAQGSLTDSFPDLLGLAED
28290	58658	A	28462	3	278	HEAAMSMLRLQKRLASSVLRC GKKKVWVRPL*TNEIANANSR QQIRKLIKDGLMRTPTAHSWP SCRTNTLSRRMGHS*SLRTLLD PVNM*GLLNASWITKC*LLDPV NM
28291	58659	A	28463	1	1043	
28292	58660	A	28464	185	804	VTSGCGKKKVWLDPNETNEI ANANSRQQIPEASSKMGLIIRK PVTVHSRA/RCPVKTPLARRG RGRATWGIR*GGKGYKPNARN AQRKFTWMRENGGL*TRGCL RKIPVNPCKDRIANMY\HSLLE G*RGNVFKNKADFSWEHIHKL EGRQRPRKKAPWLTQA*GPAG S*DPRKPRKRR*RAPPRPKKEI HQRLFSKEEETKK
28293	58661	A	28465	221	350	GPSSFRLPTLSSLHVSHGREET* HSLET*RDAVSLRIFKSLSV



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28294	58662	A	28466	598	1921	TPIHNCFKENKIPRNPTYKGCEG PLQGELQTTAQGNKRGYKQME EHSMLMGRKNQYRENGHTAQ GNLQIHAIPIKLPMFFTELEKT TSKFIWNQKRARITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYLYQNRDIDQWNRTEPSEMT PHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKI.KLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS KTPKAMATKDKIDKWDLIK.LK SFCTAKETTIRVNRQPKKWEKI FATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRIHFSKE DIYAACKHKMKCSSSLAIREM QIKTTMRYHLTPVRMAHQKSG NNRCWRGCGEIGTLLHCWWD CKLVPHILTHRWE LNNEITWTQ EGEYHTLGTVVGWGEGGGIAL GDIPNAR
28295	58663	A	28467	1	1863	
28296	58664	A	28468	2	1308	

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28297	58665	A	28469	1	1901	MPESPTPLLGRDILAKAGAIHHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFPYQRQYPLRPEAQQLQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPAVPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNQQEQCHQATQV LLNVLATCGYKVSQKQAQLCS QQVKYLGVKLSKGTRALNNEE QIEHNCQQVIAQTYATRGLLE VPLTDPNLSLYTDGSSFVEKGL QKGGYAVVSDNGILERNPLTPG TSAQLVELIALPRALELGEGKR GSSESICFLSFLVPPMTIYTEQDL YNHVVPKPRNKRVPILTFVVG GGLGGLGTGIGGITTSTQFYK LSQELNGDMEWVADSLVTLQD QLNSLVAVVLQNRALDLLTA KRGGTCLFLGEECCYYVNQSGI VTEKVKEIRDQIQRAEELQNT GPWGLVSQWMPWILPFLGPLA AIIILLFLFGPCIFNLLVKFVSSKI EAVKLQIILQMEPQMMSMT/KI YHGPLDQPASPCSDVNDIKGTP PEEISTAQHLLCPNSAGSS
28298	58666	A	28470	1	432	
28299	58667	A	28471	1	4314	
28300	58668	A	28472	1	330	
28301	58669	A	28473	1	1425	
28302	58670	A	28474	3	1110	NEEQIEHNCQQVIAQTYATRGD LLEVPLTDPNLSLYTDGSSFVE KGLQKGGYAVVSDNGILERNP LTPGTSAQLVELIALPRALELGE GKRGSSSESICFLSFLVPPMTIYT EQDLYNHVVPKPRNKRVPILTF VVGAGGLGGLGTGIGGITTSTQ FYYKLSQELNGDMEWVADSLV TLQDQLNSLVAVVLQNRALD LLTAKRGGTCLFLGEECCYYV NQSGIVTEKVKEIRDQIQRAEE LQNTGPWGLVSQWMPWILPFL GPLAAIILLFLFGPCIFNLLVKFV SSKIEAVKLQIILQMEPQMMSM TKIYRGLDQPASPCSDVNDIEG TPPEISNAQPLLCPN*AGSSWS SRRPTSPTALGFSC
28303	58671	B	28475	1	1989	

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28304	58672	A	28476	1	1280	MGNITADNSSMSCTIDHTIHQT LAPVVYVTVLVVGFPANCLSL YFGYLQIKARNELGVYLCNLTV ADLFYICSLPFWLQYVLQHDN WSHGDLSQCVC GILLYENIYIS VGFLCCISVDRYLAVAHPPFRFH QFRTLKAAVGVSVVIWAKELL TSIYFLMH EEVIEDENQHRVCF EHYPIQAWQRAINYYRFLVGFL FPICLLLAS YQGILRAVRRSHGT QKSRKDQIQRLV LSTVVIFLACF LPYHVLLL VRRYWEASCDFAK GVFNAYHFSLLL TSFNCVADPV LYCFVSETTHRDLARLRGACLA FLTCSRTGRAREAYPLGAPEAS GKSGAQEEEVTKFEGGRNGHT AKKSPCNSVQDFTGIKAVKLQI VLQMEPQM QS\KLKIYSRPLDR PASPCSDVNDIEGTPPEEISTAQ
28305	58673	A	28477	1	717	
28306	58674	A	28478	2	409	
28307	58675	A	28479	1	675	
28308	58676	A	28480	227	399	
28309	58677	A	28481	332	436	
28310	58678	A	28482	980	1399	
28311	58679	A	28483	132	218	RINLMHFRN*TSQQALSLSYNL FLMQRH
28312	58680	A	28484	1	34	
28313	58681	A	28485	985	1170	
28314	58682	A	28486	1	1203	
28315	58683	A	28487	505	716	REPCPV SQREVWRPGCLD/HCP RQSGSLGETLRGTAE/QPWP HS QVLSNLRVLQLPLISLPSLRRA LFPA A
28316	58684	A	28488	1	998	
28317	58685	A	28489	477	955	TPIHNGFKENKIPRNPTYKGCE GPLQGELQTTAEGNKRGYKQM EEHSM LMGRKNQYRENGHTA QGNLQVQCHPHQATNDFLHRI GKNYFKVHMEPKKSPHRQVNP KPKEQSWRHHTT*LQ/YTTTRL Q*PK*HGTGKTEI*INGTEQSP QK*CRISTTI
28318	58686	A	28490	37	430	
28319	58687	A	28491	507	829	
28320	58688	A	28492	643	945	CALLHSLPQHCVQHPYRSYTHR MASCRWKWGHCHSGIKMYSIP WYSTPMEGKALGDAHPQIAHS H*GAAFL*ALY*EKS*SMANRL WYSRL*PLAGDGRRE
28321	58689	A	28493	1092	1346	

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28322	58690	A	28494	173	527	
28323	58691	A	28496	566	895	
28324	58692	A	28497	76	302	KGNLSPSPALPCSLKYPFYD HRTKFTLTTPFSHTLAQKENQ SPLKHMGGKRLQNIFLPIRP*DQ TPWLLERS
28325	58693	A	28498	921	1008	
28326	58694	B	28499	1	2169	
28327	58695	A	28500	455	523	YPLYHFLHLFDSSLFSSLLVLL VVY*FC*SFQKTSSWIHYFFEGF FVSLFPSVLL*F*IF
28328	58696	A	28501	876	1061	LLPQFQSLLLVIYSEIQLLPGLVL GGCMCRGIYPFLDFLVYLHRG VYSIL*W*FVFLWDWW
28329	58697	A	28502	74	445	IALIILRYVPSIPRLRVFSMKSC *ILSKAFSASIEIIMWFLSLVLFIC WITFIDLHMLNQPCIPGMKPT*L WWISFLMCC*IWFAILLRIFTS MFIRDIGLKFSFFVVSLLPGFGIK MMLAS
28330	58698	A	28503	1	957	
28331	58699	A	28504	41	412	IALIILRYIPSIPSLRVFSMKGC* ILSEAISASIEIIMWFLSLVLF1*W ITFIDLHVLNKPCIPGMKPS*SW WISFLMCCWIWFAILLRIFASM FIRDIGLKFSFFVVSLLPGFGIRM MLAS

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28332	58700	A	28505	1	1699	MDEFLDTYTLPRLNQEEIESLN RPITSSIEIAVINS LPTKKCPGPD GFTAEFYQRYKEELVPILLKLIQ TIEKEGLLPNSFYEATNILIPKPG RDTTKKENFRPISLMNINAKILN EILATESSIKKLIHHDQDSFIPGM QGWFNICKSINVIIHHINRINNKN HMIISVNAEKAFDKIRHLFMLK TLIKLGIDETSLKTVRAIYDKPT ANIILNGQKLEAFPLKTGIRQGC LLSSLLFNIVLEV LARAIRQEKEI KDIQIGREEVKLSLFADDMIVY FKNPIVSAQNLLKLIGNFSKVS YKINVQKLQAFLYTNNRQTESQ IVSELPFTIAAKRIKYLGIQLTRD VKYLFKENYKPLHKEIIEDTNK WKNIPCSWIGRINIMKMAILPK VIYRFNASPIKLLLNFFTELEKN CLNFIWNQKRAHIAKTILSKKN KAGGITLPDFKLYYKSTVTKTT WYWYQNRVIDQWNRTEASEIT PHIYNHLIFDESDKNNQWGKDS LHNK WY WENWLAICRKLKLD SFLTHYTKINSRWIKDLNAGSKI QY\HADRTKSRERRAIASSYVSS
28333	58701	A	28506	2	1689	WRAWGRGATRRSSCHRRQSAPS LSRVGRSSQIRSALSAASGLWR RKPASAKFGRPRTGSLHLPVK* KAFVSLQESSA*MNLRQ*PE*D WISWIN*QNFGN/CQGSTLKIPV VERKILDLYALSKEHSFSPATEQ SWTENDFDELREEGFRRSDFSE LKEEVRTHRKEAKNLVKRLDK WLNRRITSVEKSLNDLMELKTM AREQLRDECTSFSSQFDHLEER KYKLPSENKHLIYANKLENLEE MDKFLETYTLPRLNQEEVESLN RPITGSEIAIINS LPTKNSPGPD RFTAKFYQMYKEELVPFFLKLF QSIEQEGILPNSFYEASIIILIPKPG RDPTKKENFRPISLMNIDAKIFN KILANQIQQHIKLIHHDQMGFI PGMQDWFNIRKSINVIIQHINRT KDKNHTIISIDA EKAFDKIQQCF MLKTLNKLIGDGTIVKIIIRAIY DKPTANIILDGQKLEAFPLKTST IQGCPLSPLL FNIVLEV LARAVR QEKEIKGIQSGKEEVKLSLFAD DMTVYLENPIISAQNLLKLKSN FSKVSGYKINVQKSQAFLYTNN
28334	58702	A	28507	1	1428	

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28335	58703	A	28508	211	506	ILSKAISASIEIIMWFLSLVLFIC WIMFIDLRMLNQPTPGMKPT* SWWISFLMCCWIRFASILLRIFA SMFIRDIGLKFSFFVVSPLPGFGIR MMLTS
28336	58704	A	28509	765	950	LLPQFQNLLL VYSEIQLLPGLVL GGCMCPGIYPFLD FLVYLHRG VYSIL*W*FVFLWDQW
28337	58705	A	28510	778	981	SQKEWYQLLFVPLVEFGCESIW SWAFFGWAQAINYCLNFRITCHW SIQRFNFFLV*SWEGVCVQEFIH FF
28338	58706	A	28511	1761	1841	CLQLCSFGLGLSWQCGLFFGSI* TLK
28339	58707	A	28512	1	1641	
28340	58708	A	28513	1	2307	
28341	58709	A	28514	1	3793	
28342	58710	A	28515	178	674	ERPRIMDLAGLLKSQFLCHLVF CYVFIASGLIINTIQLFTLLLWPI NKQLFRKINCRLSYCISSQLVM LLEWWSGTECTIFTDPRAY\SS MGKENAIVVLNHHKFGN/IDFLC GWSLSERFGLLGVSQKCIPPCL THFFGSAPPLVFLLLVIQNLQKN QQSFYLMKWS
28343	58711	A	28516	609	707	CLQLCSFGLGLTWRCCGLFFGSI* TLKYFFPIL
28344	58712	A	28517	1	2167	
28345	58713	B	28518	65	2652	
28346	58714	A	28519	267	703	
28347	58715	A	28520	3	115	
28348	58716	A	28521	2	317	
28349	58717	A	28522	1	2577	
28350	58718	A	28523	1	669	
28351	58719	A	28524	1	1089	
28352	58720	A	28525	91	507	AGTASASPAPNRSLSGSEPTSSS VTQENGADVQGHVPWKAR SRRFCPMEGTFRKVPSHGSHVP EVSMLWKACSGSFRPVEGHSV RCALTPASGCSP*AGTASASPAP NRSLSGSEPTSSSVTQENGADV QGHVPWKARSRRFCPMEGT FRKVPSHGSHVPEVSMLWKAC SGSFRPVEGHSVRCALTPASGC SPSKSKATVGCRCSDFCTVEEF LQKIFLQVESLDRRPRCLPLT
28353	58721	A	28526	1	1213	
28354	58722	A	28527	130	211	KPHYAAHGQPFTAE*RPGTDNR ADNRQ

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28355	58723	A	28528	793	1382	NTTAAGRVIRLTSENGSHTTFR YDVLDRLIQETGFDGRTQRYH HDLTGKLRSEDEGLVTHWHY DEADRLTHRTVKGETAERWQY DERGWLTDISHISEGHRVAVHY RYDEKGRLTGERQTVHHPQTE ALLWQHETRHAYNAQGLANR CIPDSLPAVEWLTYGSGYLAG MKLGDTPLV**ERPADR*ASDG ASPADGSTALAA*DQTCVQRA GAGEPLYTGQPARRGMADLRQ RLPGRHETRRHTAGGVHPRPPA PGNAAQLRPL
28356	58724	A	28529	1039	1689	
28357	58725	A	28530	1	2406	
28358	58726	A	28531	1	2928	
28359	58727	A	28532	2	1271	
28360	58728	A	28533	250	929	
28361	58729	A	28534	3	273	GKLIavigdedtvtgfallggig ELNKNRHPNFLVVEKDTTINEIE DTFRQFLNRDDIGAfrllglcw LRNRKPDHLPPLPLCAVTQCH
28362	58730	A	28535	2	415	
28363	58731	A	28536	1	690	
28364	58732	A	28537	2551	2651	
28365	58733	A	28538	2	295	
28366	58734	A	28539	1	316	CGHGGRRQSWVSRLR*CQEAAG MADSCPRSGGAILAFKSAPEVI RRALSAQSLRATSSSSASGAGA FCLSPSKYFPETSASSSATARYV LGWAASSGLLTSSQKMG
28367	58735	A	28540	1	400	
28368	58736	A	28541	257	516	
28369	58737	A	28542	1	590	EQIASDTCHLQRVVFKNISPAD AHRNLCLALRGHKTVTYLTLQ GNDQDDMFALCEVLRHPECN LRYLGLVSCSATTQQWADLSL ALEVNQSLTCVNLSDNELLG*G C*VAVHN/S*DTPSAFLQRVVV GKTGHLTEANLQGTLLLCWVF SRELTHLCLAKNPVNTGVKYL CEGLRYPECKLQTLVLWNCBIT
28370	58738	A	28543	1	2633	
28371	58739	A	28545	127	2030	
28372	58740	A	28546	1	3066	
28373	58741	A	28547	259	3222	
28374	58742	B	28548	1	2640	

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28375	58743	A	28549	2556	3662	RIPLFHYGESWNLLRADQRLIF AKSWPRASRYQQGHQDLFILRS DLPSQVVQTQNISSCRNSC*G*A CMPAGRL*RIPT*K*PANRPVKR PH*GGI*SLPGSKTYAVSVR*PD QK\SDGTLQEHDGICEIHVAKY AEIFGLTSAEPNRFQTQFRLSETK EITNPYAMRLYESLCQYRKPDG SGIVSLKIDWIERYQLPQSYQR TSPCCCHMKKDVFASTMISS SRVSNNTSKTTIKNQCQKDDS RRSLLVKNSRPAKCGSKRSCNT FLAGSLRCRSSPEHTTILRGGVR RCLQQQCEQTVRIHAKVAQK SYGNEKRLIIRPTIRVGPWSQTN NQTDDTSGTVVQSDYQTDDTS GTVVRTNNQTDD
28376	58744	A	28550	2469	2687	ELYH**HTSS*DHRQCRLMDYH CLEDNENRPVCWMALESLVNN EFSSTSDVWGLWSDAVGTHDS GPDALHGH
28377	58745	B	28551	1	1954	



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28378	58746	A	28552	1424	3807	HPLWKWLEGDMNMNIKKIVK QATVLTFTTA/LLAGGATQAF KENNQKAYKETYGVSHITRHD MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNIDS WKNAGR VFKDSDKFDANDPIL KDQTQEWSGSATFTSDGKIRLF YTDYSGKHYGKQSLTTAQVNV SKSDDTLKINGVEDHKTIFDGD GKTYQNVQQFIDEQNYTGDP EAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIERYQLPQSYQRT PDFRRRFLQVCVNEINGAVIGIP CVSIRKPDGSGIVSIKIAWIERY QPPQSYQRMPDFRRRFLQSRPA CMHDWLCAEALAWSIQTASYL VTMQVNLTSLSDDTDRLSVVS NSGWVSSGSLVRFNTIKTSSGEI KRTVPRILPDDPRSAIAEAPS EMPGHEVPVEEHFPEAGTNSGS PQGARKGDESMTKASDSSSPSC SSGPRVPKGAAPGSQTGKKQQS TALQASTLAPANLLPKAVHLA
28379	58747	A	28553	2372	3570	EALLPGDQDSQSGKGVAAREV WFLPSSFAPVLLRLVGNHHVG DNSIDSWKNAGR/VFKDSDKFD ANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHYGKQSLTT AQVNVSKSDDTLKINGVEDHK TIFDGDGKTYQNVQQFIDEQNY TSGDNHTLRDPHYVEDKGHKY LVFEANTGTENGYQGEESLFNK AYYGGGTNFFRKESQKLQQSA KKRDAELANGALGIIELNNDYT LKKVMKPLITSNTVTDEI
28380	58748	B	28554	1	2232	
28381	58749	B	28555	200	2602	
28382	58750	B	28556	1	3198	
28383	58751	A	28557	1	2169	
28384	58752	A	28558	1	2259	
28385	58753	A	28559	1	2418	
28386	58754	B	28560	1	1974	

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28387	58755	A	28561	3	2077	
28388	58756	A	28562	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG AIQAFAKENNHKAYKETYGVS HITRHDMLQIPKQQQNEKYQVP QFDQSTIKNIESAKGLDVWDSW PLQNADGTVAEYNGYHVVFAL AGSPKDADDTSIYMFYQKVG NSIDSWKNAGR VFKDSDKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGKH YGKQSLTTA QVNVSKSDDTLKINGVEDHKT FDGDGKTYQNVQQFIDEGNEGI LPISPPKQDFRLLG
28389	58757	A	28563	610	2303	SLPNLDNAAICSSSSSPTRTR*SL SEGATQ\AFAKEYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDN SIDSWKNAGR VFKDS DKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKH YGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYRGPLESPTHQAEFNPTS CVSSLGTLQGFPAPAWLAL AHP VHPLKHKSGGSNRLSAAIWGIK RKPARVCPGTGIHASSQIQGEW RTECAVGPKAKAKATAGWRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNGQSEHQTY ESIVIDSAPNLGIGTINVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFE PDVRILLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVGKGQIR MRTVFEQAIDQRSSTGAWRNA LSIWEPVCNEIFDRLIKPRWEIR
28390	58758	A	28564	1	2079	
28391	58759	A	28565	1	774	

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28392	58760	A	28566	1	2124	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKANKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFFKR GAIFRVHKAHVNPMSPKCRRPG GRQAYPLVNWEDRNGRSQKTV HTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFAKENNQK AYKET/YPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVSALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGRVFKDSDKFDAN DPILKDQTQEWSGSATFTSDGR RSLESTTTAARPIWRKDVGGDQ TQEWSGSAPFTSDGKIRLFYTD YSGKHYGKQSLTTAQVNVSKS DDTLKINGVEDHKTIFDGDGKT YQNVQQFIDEGNYTSGDNHTL RDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGT NFFRKESQKLQQSAKKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLF TDSRGSKMTIDGINSNDI YMLGYVSNSLTGPKPLNTTG LVLQMGLDPNDVTWASLEPHE SFQWVRGLASSGVKLQTSVVL QLIKAMWTQRVSSSVYCKEQ MNNASTMSKRTSAGCHCWQG
28393	58761	A	28567	1	3987	

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28394	58762	A	28568	1	1950	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDN SIDSWKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDN SIDSWKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL/VFEANTGTEEHPQPQ\ERP RTQSFTSAFAERRECIPNVPADT KLSKIKTLRLATSYIAYLMDLL AKDDQNGEAEAFKAEIKKTDV KEEKRKKEASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLTVTASQHAPPPPTHMEGFEL FHLPDLCSPSQDAQTTGRTQMK PDHSPRPSHRVPQAKGNV VIT SYM TNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQQQLTV
28395	58763	A	28569	2	1778	
28396	58764	A	28570	1099	2224	DGQQIALHRLALRELQQAVH AGLPQQAKILFDGGSE/TRQNPL QQLVHMGLPRPLDKKNFQEP
28397	58765	B	28571	1	1938	
28398	58766	A	28572	1	2367	
28399	58767	A	28573	4659	13369	TVFRPFHVGVHLLIVDSCSKL EQHSTLSRAILLIYKGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTGKRAVSATQLMDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQGGEDSPNRFDDGG RKKQIRTVRQFIDEGNNTPADT QTLRDPHYVEDKGHKY
28400	58768	A	28574	6803	8521	
28401	58769	B	28575	2010	17745	
28402	58770	A	28576	1	1060	

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28403	58771	A	28577	1	3585	
28404	58772	A	28578	44	317	LKALLLTQSLFGGLLTQTRMKF GAVTRIGDLPWEINPLSSCSLL HEKDPPTTSGPQTHQPKIHLTN FKSGCSPCRAKSQFFLSLCSST
28405	58773	A	28579	98	617	KALLLTQSLFGGLFTRTRMKFG AVTQIGDLPWEINPLSSCSLLR EKDPPTTSGPQTHQPKIHLTNF KSARFKKIKACYHSPATAWPFK AYKLSLQFPHTCPKTRQALQV SSGSVPYQPNCFAYPPHGAKPI YSPILNTSLHNPLFCSGSQTCL YYSFAPFIPASLRFIILD
28406	58774	A	28580	1	1500	
28407	58775	A	28581	42	257	
28408	58776	A	28582	3	425	KTGKYD/AVIALGTVIRGGTAH FEYVAGGAS/NTLAHVA/QDSEI PGAFGVLTLLKA*TNDRAGTKL HGGWGGKCLTACRSALWADL QIRPYDHKNRGSNVHNRVPAS GAAAMAIHCLECGWAPLAAGD NVGKVCVPDAGLLPA
28409	58777	A	28583	327	1512	SYWTIHQVSLNHSYLPGGNIS SLKKMAGRNSERKTVLVKSSF QEVNRGTEALALWENGDFEAP VLTFTTALLPEGATQAFGKENT QKASKERYGSLNITRNNMLQIL NKQQTEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVVFALAGSPKDADD TSIYMFYQKVGDNSIDSWKNA GRVFKDSDKFDANDPILKDQTQ EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQNVS KSDD TLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGGVNADVGDVVVRLPVW HRRGGEAVFMQVSRLQILRIILP HGVVAVDRDHHIAHDRRRHVA GDRSGSVRL
28410	58778	A	28584	845	966	
28411	58779	A	28585	215	420	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIARCTGHIDP VTRFRPRAR*GSSHRNKAVDTQ RH
28412	58780	A	28586	464	847	

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28413	58781	A	28587	501	823	PEVQSPDVRHIPGGA*DVLPHQ GIKRPDALPGPLLHA*PDNLRC CPRSGTAAGSIHQDARLRYSVW RWGLLDRLAAVICRQSTHSRCR RKQRRALYRRDAGYLRRN
28414	58782	A	28588	335	902	
28415	58783	A	28589	404	733	
28416	58784	A	28590	2	246	
28417	58785	A	28591	466	861	
28418	58786	A	28592	122	926	
28419	58787	A	28593	171	733	
28420	58788	A	28594	1	774	
28421	58789	A	28595	1	1575	
28422	58790	A	28596	1	105	SVKLGWNGVSTYVPFCLTICSV SFFQENLHLTTCRA*PSIPPPAA RRSPKKCSP*KLRLP*LSGKSSS YNL
28423	58791	A	28597	237	461	
28424	58792	A	28598	1	1341	
28425	58793	A	28599	1	792	
28426	58794	A	28600	16	546	QLNGRSIRHEVMSHRKFSAPRH GSLGFLPRKRSSRHRGKVKSF KDDPSKPVHLTAFLGYKAGMT HIVREVDPRPGSKVNKKEVVEA VTIVETPPMVVVGIVGYVETPR GLRTFKTVFAEHISDE/CRLPL RQKKAHLMEIHVNGGTVAEKL DWARERLEQQVPVNPVFGQDE
28427	58795	A	28601	1	1251	
28428	58796	A	28602	37	1307	EFGFDGVMMSHRKFSAPRHGSLG FLPRKRSSRHRGKVKSFKDDP SKPVHLTAFLGYKAGMT HIVREVDPRPGSKVNKKEVVEA VTIVETPPMVVVGIVGYVETPR GLRTFKTVFAEHISDECKRRF YKNWHKA\KKKAFTKYCKKRQ DEDGKKQLEKDFSSMKK\YCQ VIRVIAHTQMRLPLARQ\KA HLMEIQVNGGTVAEKL\DMA REKLE\QQVPMVQVFGQDEMI DVIGGDQRAKGFKGVTRSWPT N*LPFKA\HLGLSRVACFGAW HPARVAFSARAGQKGYHHRT EINKKIYKIGQGYLIKDGKLIK NASTDYDLSDKSINPLGGFVHY GEVTNDFVMLKGCVVGTKKR VLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFQTMEEKKA FMGPLKKDRIAKEEGA
28429	58797	A	28603	1	2133	
28430	58798	A	28604	3	245	

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28431	58799	A	28605	1	1824	
28432	58800	A	28606	1	1035	
28433	58801	A	28607	1	496	
28434	58802	A	28608	1568	1793	
28435	58803	A	28609	1	1392	
28436	58804	A	28610	1	1389	
28437	58805	C	28611	104	253	
28438	58806	A	28612	114	469	VSRPTYAKVFSTTSKTAPQKVFP TAWCSA/TGHETALSATQVPIQ WIATAPNSPAPPSPRRQSWVS QIPSSATSPNFTM*EPRTQEVTE PHDSRPAIPSPAVPRRESCTGRP HLPATTP
28439	58807	A	28613	3	2196	
28440	58808	A	28614	237	348	NPVN*SQTT*TSE
28441	58809	A	28615	950	1094	
28442	58810	A	28616	146	822	LGFLRLSEMPRKQGVYRTRIW KFEDGLSNVLVI/PIEQINHMRD VFGSGSERATCLARGRGYINSL ARCQNLVNRDLHLSPQDSTL VHYIDDIVLHGFSEEEKGQVAQ SADLDEGLLKIPGDTFGPEADK DFLHKDLSTEIVGQSYNTHHM AQDSIPWNPSGQEPQVREHEAC HHLGSGSPSWELCEQGPPVTE SFQVLVTSGLDKENMAYMHCG IICSNKKG
28443	58811	A	28617	1	1791	
28444	58812	A	28618	244	416	
28445	58813	A	28619	2	1520	
28446	58814	A	28620	95	421	PVTSTSTKRTPTQKPHPKVISLK DQIHVVDKSMRKNQCKNV EKSKNQNSSSPHDHNSSP\SARA ENWTEYESDKLTEVGFRGWVI NSSELKEHVLTHCKEAQNLHN
28447	58815	C	28621	46	174	
28448	58816	A	28622	425	1291	
28449	58817	A	28623	1	1410	
28450	58818	A	28624	14	348	GLFPNKIPFSVLEIRTWAHLGR HSAHCTSCAWPQVACLPLAT HPSTCTFCSLQAPGRPGQSPLS PRRACGPEDLPPPPYV*DLAPSL GPSLGPLMSQSQPRRTPLRG
28451	58819	A	28625	96	295	PWKHPA WRQRWELCHPPFP/I RPLTAALREQPGLLGRSTTVFT LMAREPPQAAADSCLCIVQME A

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28452	58820	A	28626	105	389	CQFAHGTASSPRVCLRHRCS WQKAWAVVCCTFCSLQAPGRP GQSPLSPRRACGPEDLPPPPYV* DLAPSLGPSLGPLMSQSQPRRT PPLAWGS
28453	58821	A	28627	461	799	
28454	58822	A	28628	1	384	
28455	58823	A	28629	301	987	
28456	58824	A	28630	239	384	VLPAGAQAARSSDTRP*PEPH FSIESVFPRWIFSAFQSLNNFFQA RF
28457	58825	A	28631	1	1054	
28458	58826	C	28632	243	392	
28459	58827	A	28633	1	1104	
28460	58828	A	28634	194	863	YLLFVKNMSSLEISSCFSLETK LPLSPPLVEDSAFEP SRKDMDE VEEKSKDVINF TAEKLSVDEVS QLVISPLCGAIS/LNWKGLTENT FEGKKVISLAEYEA YLPMANE VRKICSDIRQKWPVKHIAVFHR LGLVPVSEAKP*SFAVSSAIHRA AISLKLLSYC/AFDTFKRPRVPI WKKIEIYESSTWKG NKECFW ASNTLITYVFRACNLNFVKLI.L
28461	58829	A	28635	3	338	SSPPTAPAKLRIVPLVGGIPAR WCLSVCASQCPDTRVHVFLHW WCSSLC PAPVCLSLCRGL*GHF PPDSEDQSSPNC SGYTLEEKI LRSQTIPSCNGKFCPPRRAYDG
28462	58830	A	28636	405	800	
28463	58831	A	28637	265	539	
28464	58832	A	28638	3	1116	
28465	58833	A	28640	208	350	VWLKEPSAEPAPCTWSALCGSC LLGGL*NSAFLSHRPHTSGGFFP LN
28466	58834	A	28641	563	594	
28467	58835	A	28642	245	580	
28468	58836	B	28643	1	435	
28469	58837	A	28644	673	1012	QPQVSFSSEYAIHIMRCPHISKIS SLYYFNCFRY*DCYCHTFATTS ISLVRYATGCKLIPRICVRTPRAI PVFSVTYEEKSCPVGKLN TGA WVRAWKATSTSVVHLTKWVL
28470	58838	A	28645	1171	1328	MVIGGTKNERKHIDSDEPLFPSP NSSARGRAISSTS*ALVPGVRGF LSSIPLSLTTAYPPF*SPFSS
28471	58839	A	28646	34	266	GSCS*DFLVRGAFNVINIKAWA SGPVQGS AVDL SHGLHLGLHL KNDL*FYFSN SGIDKPEIAKLSG CSFGGTFLIWG
28472	58840	C	28647	199	309	



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28473	58841	A	28648	808	926	YCYSSLDPVSLTSLLSLSPKLL L*SYKSFFKWSPRCSP
28474	58842	B	28649	107	264	
28475	58843	A	28650	301	470	EIQLVLSLSGGGYSHAVLMIVS SHKI**FYKGLFPTFALHFSLLP CEEGCICFPF
28476	58844	A	28651	2	263	WEKKDTEWRKKVILSSV*LRL VIF*PFSLM\LF SHPVWR*ARSH ESHLAITHLWALYF*PPCQICFL *DRGHQATDGLTNGTPSELN
28477	58845	A	28652	63	191	DLPWTPGPAC*PMLQC**GGAN IYARRQGADAAGDQGSSCRL
28478	58846	A	28653	1	554	MPTYCPGASLLILTYKTPKELLS IYVSTIRKSRERRRNRRLGAR NFRSEEQIYDQWRLDQVGKFFP FPRPRENYHFGSEHVGSFSLDK CCNEKLYEVIDLHLKKKFLNTE TSLVKCEVSRWVTLNLLLPY H/VLFQI*LSWRERQNSCKTTN GSSNGAPDAVHN*NLLWSLGP AC*PMLRC
28479	58847	A	28654	3	317	SRRLPFSLICMAKHWLPALPEN GYMKQFCVSGLGVLFHGCVFL CWHHCCFVL*VWSLGSPPSRG LHLVKAFFLCYPRSNCFLLNWG IVGVVQLRFPQEGCLWCH
28480	58848	B	28655	1	400	
28481	58849	B	28656	49	492	
28482	58850	A	28657	1	917	TALETAPTLALPVSSQPFSLHTA EVQGCavgiltQGPGCPVAF SKQLDLTVLGSPSCLHAVASAA LILLEALKITNYAQLTLYSSHNF QNLFSFSLTHLSAPRLQLYS LFVESPTITILPGPDFNLASHILD TTPDPDDCMSLIYLTFTFPFHISF FSVPHVDHIWFTDGSSTRPDRH SPAKAGYAIESSTSIIEATALPPS TTSQQAELIALTRAFTLAKGLH VNIYTDSKYAFHILHHHAVIWA ERGFLT/IARVLHH*CLFNKNSS QGCFTSKGWSHTLQGPCKGV RSHYSRKCLC
28483	58851	A	28658	3737	3886	
28484	58852	A	28659	349	1775	
28485	58853	A	28660	1	1194	
28486	58854	A	28661	1	704	
28487	58855	A	28662	41	275	
28488	58856	A	28663	159	1504	
28489	58857	A	28664	275	552	
28490	58858	A	28665	178	619	
28491	58859	A	28666	3	369	

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28492	58860	A	28667	1	340	
28493	58861	A	28668	516	734	WTGDWRRTCDRENQHVSGAARTAFIPTNGAISPGINYSPGH*Y*DCHLPQA*P*LCRAAGQNRCHVARTCLG
28494	58862	A	28669	1	1163	MHTHARETCLALGKPADDATLTAAIEAVGLENAARVLKLYPFEMSGGMLQRMAMIAMAVLCESPFIIADEPTDLDVVAQARILDLESIMQKQAPGMMLLVTHDMDKWGRIADVESQYRYQTTPNPKIFAGGDAVRGADLVVTAMAEGRHA AQGIIDWLGLDVKLGALAEERRKVLQVKTENLQAERNRSRSKSIQAKARGEDIEPLRLVKNLGEELDAAKAELDALQAEIRDIALTIPNLPADVPVVGKDENDNVEVSRWGTPREFDFEVRDHVTLGEMHSGLDFAAAVKLTGSRFVVMKGQIARMHRALSQFMLDLHTEQHGYSENYVPYLVNQDTLYGVGLYPLGALASGW/WALASGWLPKRERKD/GDTGAHGVPRGSRKPRIARKVRGT
28495	58863	B	28670	1	4770	
28496	58864	A	28671	1069	1398	VIGAQPVLRIIRKQARRQINRLTLILLHYCLTTKLKNGVKPGIVAAFYFLPGAG*IHPAGCHGTQL*SFGKMRVQYTRVTLSSQQASGKISAYLIDLKPLLKLIHCGVH
28497	58865	A	28672	4246	4453	
28498	58866	A	28673	1	1185	
28499	58867	A	28674	723	878	
28500	58868	A	28675	1085	1246	
28501	58869	A	28676	1	1254	
28502	58870	A	28677	1	2175	
28503	58871	A	28678	340	994	
28504	58872	A	28679	37	261	TITPAGRRMHCKGACMKPLLDVLMILDAVRELE*TITPAGRRMHCKGACMKPLLDVLMILDAVRELEKQAIKLHEGWENELVIGVD DTFPFSLLAPLIEAFYQHHSVTR
28505	58873	A	28680	410	896	WAWAASAVQPRSIWQ/GAGVG NLTLDDFDTVLSNLQRQTLHS DATVGQPKVESARDAPHIAITP VNALLDDAELAALIAEHDVLVD/WYG*RCGT*STERQQR*RG*RSAPAMTAHDRDAIASSSETCARSRWSVEYASPVCAAPPDSRSKR RSASNSAASHVF
28506	58874	B	28681	1	2298	

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28507	58875	A	28682	1915	5313	
28508	58876	A	28683	1	4221	
28509	58877	A	28684	1	1007	MAALQMVNGQK WVSSNQKY WL VYKTTDPRLRP IFSGYQPM CPFNGRPFWIHKNP MG VHWAV ATGLALIPVIGIAEFGWFWFGG ETYMAA WNVSLGTFTGAIQST FNVTLWSFIGVESASVAAGVVK NPKRNVPIATIGGVLIAAVCYV LSTTAIMG MIPNAALRV SASPF GDAARMALGDTAGAIVSFCAA AGCLGSLGGWTL LAGQTAKAA ADDGLAFPPIFARVNKAGTPVA GLIIVGILMTIFQLSSISP NATKE FGLVSSVS VIFTLVPYLYTCAAL LLLGHGHFGKARPAYLAVTTIA FLYCIWAVYITHIDACVVVYIA GYRAAKLTCA
28510	58878	A	28685	867	1681	
28511	58879	A	28686	865	1290	RWWENRLFRKNPARAQKMVL PERFG*SAYPNGFAGTWRLDKL PIAQIHAHMIGYLAAVDMEKQ QISPAQVVVRHNRCPAIVVHLI GRARELSLKDLVVG IKNQPATV KAFIRPRTAPDVRLAKLLLQAV NRHFGNVMMQMVAA
28512	58880	A	28687	1	709	
28513	58881	A	28688	2	657	LMWALPKVTRGPVYMAGSPQT AFIQVGPRVHAHLQPRAAPL*A GEVWKPRLVGRSHWASRPSA LQKGEPGSPSWENACVPQAPH RLLHQQKAF
28514	58882	A	28689	3	227	NSQDFPACGGLCHAE LDR TAA GLVHQH\RHPGHTSVAAEKLCH GDVEGDGCNGPASD/PGYI*GQ AAPAPLPDLL
28515	58883	A	28690	1227	1719	
28516	58884	A	28691	1	1701	
28517	58885	A	28692	15	3298	
28518	58886	A	28693	1767	1998	YCDTTHNSYLLYDSVCRGYAR AVWRYQTDIAANLE*RRLP SGA GKSDWSSGDSEKAKTAAHTIY RDAGRRVRGYRQL
28519	58887	A	28694	1	370	

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28520	58888	A	28695	1	910	MDKERIIQEFVPGKQVTLAHLI AHPGEELAKKIGVPDAGAIGIM TLTPGETAMIAGDLALKAADV HIGFLDRFSGALVIYSGSNYTL ARKTQAVEFNDKGDIDTPGEYF NHPRWYHALITTLQDQDMLSP LIWGFRNYKDVQVIKATPHKIV ILMGILLSPSVFATDINVEFTAT VKATTCNITLTGNNVTNDGNN NYTLRIPKMGLDKIANKTTESQ ADFKLVA/MGAAVASVGLIPL* PEMHHAHLSELLYRSLVIHLRR QVISVWVSKNGLLMMPLSLNL TVRKRYAGAQTRCSPIRVLK
28521	58889	A	28696	605	2021	
28522	58890	A	28697	2256	2336	CIKCCARRIAREPGYLFS**RCK YPG
28523	58891	A	28698	1802	4488	TLLRQGSNFLMTRRCATKSWN V*SWIKSS/MQMGQKMGVKISD EQLDQAIANIAKQNNMTLDQM RSRLAYDGLNYNTYRNQIRKE MIISEVRNNEVRRRITILPQEVES LAQQVGNQNDASTELNLSHILI PLPENPTSDQVNEAESQARAIV DQARNGADFGKLAIAHSADQQ ALNGGQMGWGRIHASLPGIFA QALSTAKKGDIVGPISSGGRFD GTVEVKDGHILVNGKKIRVTAE RDPANLKWDEVGVVDVVAEAT GLFLTDETARKHITADTPAALR WLEENQLEDGHECLLRVISSD GRSRGFINGTAVPLSQLRETSTT TGARRVIRAIRRINSSDASTIPTL MAITISNNTVSDMHSSMTMMS TRJRTLITTIYNGDLRMIRQRKL CKTAIARTYGNDDTFHPGMRH QRMHRVFKNAPHLDPVVTLN IYPKADESSSLKASRGTRGAAY RPARQNLYSASSGKKDENPVIE FKNVSKHFGPTQVLHNIDLNIA QGEVVVIIGPSGSGKSTLLRCIN KLEEITSGDLIVDGLKVNDPKV DERLIRQEAGMVFFQFYLFPHL TALENVMFGPLRVRGANKEEA EKLARELLAKVGLAERAHHYP SELGGGQQQRVAIARTLAVKH KMMLFDETTDFDPELVHEVL KVIHEFAEKGITNDSL TENPAKT QGECCGLQSQERGPQREPTPRH
28524	58892	A	28699	1	2307	
28525	58893	A	28700	3	976	

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28526	58894	A	28701	2	136	YLSAV*FCSPGQPPSALLVCGR RGYWCLWPLSSCHLTLLRCVS
28527	58895	A	28702	1	608	
28528	58896	A	28703	222	329	
28529	58897	A	28704	387	728	
28530	58898	A	28705	1	1184	
28531	58899	A	28706	478	627	
28532	58900	A	28707	33	1072	
28533	58901	A	28708	35	516	RVVEFADEGQGPAALSLWSGS SPETLKLHWPVHVN*IRFSSWK TFRIRSRDFWADRLMRTLLRNF LSKWDHL*GQTLGVSLRRV*NE GSSPCHTPRPSAVLPPVLLDGG R*THMKLHAASSRGWLRTRLT ELEYSLVIRIRRDGGLAGLRGN SGAQQGDA
28534	58902	A	28709	1	777	
28535	58903	A	28710	531	704	
28536	58904	A	28711	294	617	
28537	58905	A	28712	804	1020	HFLSGGRRQRPPRWTIVA*SPR* PRCRCWGS*RPGRGALPQPR S*WHPSGSARGRHSGSGLETSG PTVS
28538	58906	A	28713	102	510	PWPHTGGRRQRPPRWTIVA*SP R*PRCRCWGS*RPGRGALPV VRKQPGDPKTPLASCEPNQPV PEPAAAPTRQSKRLCYLSHVAD GILQVQARGRHSGSGLRRLGR PSHEGPWLKGTSCRSGTTCDR PWV
28539	58907	A	28714	2	1580	
28540	58908	A	28715	286	352	
28541	58909	A	28716	1	531	
28542	58910	A	28717	1	1440	
28543	58911	A	28718	238	567	FGDAGKFDGKFSSHSKLLSGFD AWTELALNHRFLLQLVEVLPE ANRQLRQSGAGDGGQAVF*F HRFLASVHQHKAASASPPYLFR IKCPVPRLRKAPALLLIDNRLYG
28544	58912	A	28719	1	3534	
28545	58913	A	28720	1846	2121	
28546	58914	A	28721	176	462	TSRHSVYISDTELKPRKSSKPTF CGCDSLFPICHP/HGLSDVALI VQQLRQRG*PLQPARLPVHWR HQNAVVDGVLSGENGGAGWG RAWLRIRRS
28547	58915	A	28722	225	3465	
28548	58916	A	28723	937	1770	
28549	58917	A	28724	142	484	

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28550	58918	A	28725	1	1521	MIPITWPKFAELHPFCPPEQAEG YQQMIAQLADWLVLKLTGYDA VCMQPNPGAQGEYAGLLAIRH YHESRNEGHRDCLIPASAHGT NPASAHMAGMQVVVVACDKN GNIDLTDLRAKAEQAGDNLSCI MVTYPSTHGVYEETIREVCEVV HQFGGQVYLDGANMNAQRRD MAGKPGPLTVRKMRGSRVTVR AL*/ASVWIGFDDHRRNLGHTT ASGAIKDQISGYEGGAKSAQPA WDA YMKA VLEGVPEQPLTPPP GIVTVNIDRSTGQLANGGNSRE EYFIEVNEIVNPNATLDWQLA LRQAAGKTDLARDMLQMLLDF LPEVRNKVEEQLVGENPEGLV DLIHLHGSCGYSGVPRMKNL CQLIEQQLRSGTKEEDLEPELLE LLEMDNVAREASKILGGHDN GGNALLHKALPPGNVGKWAM APIPPFPQPGKSVTICWKPASS ENRSNLEIFLRELISNASDAAD KLRFRALSNDLYEGDGELRVR VDEVLSPASVPYS
28551	58919	A	28726	1	1279	
28552	58920	A	28727	3	762	
28553	58921	A	28728	1	1472	MTQDELKKA V GWAALQYVQP GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG YSRSGGGTASHGSPKSWAIGSL GRFGNEYSGWFDLQLKQRVYN ENGKRVDVVMMDGNVGGQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFVVGK HGAPKIEIQMLDWKTQRTDAA AGVGLENWKVGP GKIDIALVR EDVDDYDRSLQNKQQINTNTID LRYKDIPLWDKATLMPRIPTQR YGLAKA/SLEAD/VRY/MANAM GPEGVRVNAISAGQTRTLAAPG IK\DSRK\MLAHCEPVTPIRRTVT IEDVGNSAAFLCSDLSAGISGEV VHVDGGFSIAAMNERDPFTDL HRYRMNLNMMNYGAQRNM

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28554	58922	A	28729	2	419	RPRPRPRHMLQGTHRQRHLHA GPGVARRRWGGMARRAARGR PRLRLCIFSRSRQLGLRLRFLSST VNEGDQVKTV\RSGHFCGGLS SFSFSSSFSSGKKRPSNSPGSMR LGSPPSGAGRAGGIIVTAC*AR LSTCNTKQ
28555	58923	A	28730	725	2804	
28556	58924	A	28731	661	1218	DVREGDRDPFMIKVHSCVFVDF AKTMHDGA/SVSLRGNLISHKG EDRY/VFRDKSGEINVVIPAA/V FDGREVQPDQMINISGIADKLP VIAPTNATSKLKLASQPEDDSEI YDGCNGAQPGDYWFAAFVSG MFSRWLAKTILSRHILSVTIRSC KNGEWLAVGGAENGAYSDSR VAVMLLLSAWGLFDF
28557	58925	A	28732	1	624	
28558	58926	A	28733	1	1281	
28559	58927	A	28734	114	266	
28560	58928	A	28735	1487	1570	
28561	58929	A	28736	1	3402	
28562	58930	A	28737	1	2466	
28563	58931	A	28738	372	647	SGWSWNTKFPTGGFRWPAQPG TELESSQPR*LVMPTTSPFRAL DVCEYLPACVAVISGCHPSRFA RSYVSAPD*QNVQLTYPHIVLN RHL
28564	58932	A	28739	1	2235	
28565	58933	A	28740	3	293	
28566	58934	A	28741	737	963	
28567	58935	A	28742	3	282	RRLRASGCIDKLPSG**YARPAR *DPAPGFR*STPVRKCDQTRSPA MKVIAAADRKLWCGAICPLSA KPPAGRAPNAPAASP NRPM T PSL
28568	58936	A	28743	2	289	
28569	58937	A	28744	1	1662	
28570	58938	A	28745	421	2634	
28571	58939	A	28746	134	954	
28572	58940	A	28747	1036	1383	
28573	58941	A	28748	2	589	
28574	58942	A	28749	1	801	
28575	58943	B	28750	14	499	
28576	58944	A	28751	3	916	
28577	58945	A	28752	3	589	
28578	58946	A	28753	1	1675	
28579	58947	A	28754	1	522	

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28580	58948	A	28755	1229	1660	LMVSGFLTSPKDHRIIVAKPEQ FWKLRQVMFMAIVISLPTIGER FSPFLLKSPLIRPSRCGTTDFISG LTARPEFSQSRMVLIAASTITSL MCAGSFLPIRPLASICSLNATTS **LPFSSGRDSSRKRRRTQAITCSP RCGS
28581	58949	A	28756	1	230	HAVCLAAVHFSSWALNNSETF NSIWSCASAILGNLGILTGSPPL ALCRTLCITYPI*CPRDAKALR RPRECVRHD
28582	58950	A	28757	1	850	MPVMFLASLSGKHQGHHPKG ERGKFKIKERGTVATEDRRSGD STFYAIQPTRRQKR VYGLALLL QLHRRRQNLNIDSVSSVGLAAL VTAFIGVDFDFANGEQTSQPLW TWMSVGDFNIGFNLVLDGLSLT MLSVVTEGYSR*EHRPTPSQPR YISSRLSASTRTTM/PGDEQVGV SEEARVALSDHREHGQRQAVQ HQVKTDVKVAYRHRPQRLAV CLLAVSEEINADKGGYQRRQA HRAY
28583	58951	A	28758	20	282	
28584	58952	A	28759	38	966	RDGLESRGRVCSLRTAFQRSSS EAFTSDLQAAELQNRASNRPAR IGHAHLVIFPVQSSWM*RKLAS PRNNLVIPQEKALKEYIKIGNLV MSLAAAPLNR*GLL/IEWNDND GGCKGACDRVPHQNVTA LNLR DQCINGECYDEVLFHGLEEYIN NLQGDGVIVLHTIGSHGPTYYN RYPPQFRKFTPTCDTNEIQTCTK EQLVNTYDNTLVYVDYIVDKAI NLLKEHQDKFTTSLVYLSDHGE SLGENGIY LHGLPYAIAPDSQK QVPMLLWLSEDYQKRYQVDQ NCLQKQAQTQKDCVLLIFAKQ
28585	58953	A	28760	1120	1335	
28586	58954	A	28761	846	1245	TVRKRGRTRHPHGSRRTL SLPLR HSSDR CNRTRSADRSTGPRL/A QPRYISSRLSASTRTTMPVTES MVSDRPSSTR LKPKLSPTDIH VHSGWLYVCSPVAKKSTPMKA GTTAGRPTEPTPTIATSGLNALL
28587	58955	A	28762	265	1179	
28588	58956	A	28763	188	322	



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28589	58957	A	28764	1	3114	MLQQDSNDDTKDVSLFDAEEE TTNRPRKVKIRHPVASFFHLFFR VSAIIVCLLCELLSSSFITCMSKK WLAVVIVGVVLQGANLYGYLR CKGQEVRETFAEPSLQATQMK LKRARLADDLNEKIAQRPGPM ELVEKNILPVDSSVKEAIIKTL KIYYLGAPAEAATKEDERTTSG PGHHATNYHFLKFDLYLSWL HFVHKDAILSGHPLVRLSTRV LRGPNDFHGVSSVDSVLAIFV LAEPMGSLASLEN
28590	58958	A	28765	1	3219	
28591	58959	A	28766	3	245	
28592	58960	A	28767	2	1193	CANQLRDCLVIPTITGLVRLVV AGANGDRLGQPVGTADVRI.SR CRKVMPSRSVEMGLVPSSSVIV TVLPLIGFVLLAFSRGRWSENV SAIVGVGSVGLAALVTAFIGVD FFANGEQTYSQLWTWMSVGD FNIGFNLVLDGLSLTMLS SVTG VGFLIHMYASWYMRGEEGYSR FFAYTNLFIASMVVLVLADNLL LMYLGWEGVGLCSYLLIGFYY TDPKNGAAAMKAFVVTRVGD VFLAFALFILYNELGTLNFREM VELAPAHFADGNNMLMWATL MLLGAVGKSAQLPLQTWI.AD AMAGPTPVSAIHAATMVTAG VYLIARTHGLFLMTPEVLHLVG IVGAVTLLLAGFAAL*Q*K*HP RHPKHRNAG**TRVLQRGAGC AGAIRVTDHFRG
28593	58961	A	28768	3	2191	
28594	58962	B	28769	1	2263	
28595	58963	A	28770	1089	4965	
28596	58964	A	28771	41	249	
28597	58965	A	28772	533	709	VSFLIVSSSLIALWSEKQFVHSV LLHLLRSALLPTMWSILE*VWC GAEKNVYSVDLG
28598	58966	A	28773	2714	3599	LGSQWH*IKLPWAVWSFSQY
28599	58967	A	28774	45	188	GKVQCHRGGLIHVNWLPPVKKF *LRQKGKPTSSSQETPKTEPGRLLKP
28600	58968	A	28775	722	856	GNDLCPKTIRTGDWCVPGGT RKSAWK*GKISGSLSFPLVRDG

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28601	58969	A	28776	474	1338	PANQKKPRTRWIHSRILPEVRR GAGTIPSETIPNNRKGGNPP*LIL *GQHHPDTKTWQRHNKK*KFQ ANIPDEH*CENPQ*NNGKPNPVE HSKKLIHHNQVGFISGMQGW NICKSINIIHHINRTNDKNHMIISI DAEKAFDKIQHPFMLKALNKL GIDGTHLKIIRAFDKPTANIILN GQKLEAFLKTDTRQGCPLSPL LFNVVLEVLARAIRQEKEITGIQ IGKEEAPQKQQLFCRYYYHGK RAPQLLITHLEEDDEWDIIRYY NVMSEEEIKRMKEIVKPKII
28602	58970	A	28777	2289	3225	LTNQNKSRTRWIHSRILPEVQR GAGTVSSETIPNNRKRWTPP*LI L*GQHHPDTKTWHRHNNKRRKF QANIPDERQCKNPQ*NTSKPNP AAHQKAYP**PSQLHPWDARL VQHMOTNKHNP SHKQNVHDKN HMIISRDAEKSFNKIQPFMLKT LNKLGISGTYLKIVKMHTMSSS HLFYALCLLTFTSSATAGPETL CGAELVDALQFVCGDRGFYFM EQCTMAVSIRGRELLGPSEQEM LHKESGKQRQKANTIPVTSKIV HLALYATLLL FVMEQFLGESHK SREIFSFEQQISELGKESMKFSEE KEKE
28603	58971	A	28778	1177	1272	
28604	58972	A	28779	480	766	SSEIQHWFQGGQPRWSRCRVSGR RHEASTVLPLCFLLPQNSSSMQ LG*NRSMP/HVSESSRTLVL*EV TKHQVSSNFKMRDKDRSGRAS SLRKHRRE
28605	58973	A	28780	1	1344	

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28606	58974	A	28781	971	2314	PTNQKKSRTRWIHSRILPEVQG GAGTIPSETIPINRKRNPPL*LIL* GQHHPDTKAWQRHNKKEEL*T NSPDEH*CKNPQ*NTGKPNP\EH IKKLIHHDQVGFIPGMQGWFI HKSINVIQHINRTKDKNHMIISI DAEKAFDKIQQPFMLKTLNKL GIDGTYLKHRAIYDKPTASHLN GQKLEAFPLKTGTRQGCSLSLF LFNVVLEVLARAVRQEKEIEGI QLGKDEVKLSLFADNMIVYVE NPIISAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTKSQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIAKTILSQKNKT GGIMLPDFKLYYKPTVTKTKW YWYQNRDIDQWNRIEPPPIISHT
28607	58975	A	28782	148	287	VLHSYAI*IASALKVGISRHHP* GSIPSRSLLVATTPTRGVTAAL
28608	58976	A	28783	1	1938	
28609	58977	A	28784	1389	1499	
28610	58978	A	28785	1	351	
28611	58979	A	28786	1	329	KNLDEKLLPASSSSCRIWATSP VHHLWQVLKKILF/GLEPYEIST LFEQRQAM/LQSIKEGVVAVDD RGEVTLINDAAQELLYHNHNFIR SRSLPVFVLASACGSGTRRRRA
28612	58980	A	28787	1	419	VRPGHLLDIDDTDMPSLRYS EAQRIGQPFKGDDILKALNGEE NVAINRGFLAQALRVFTPIYDE NHKQIGVVAIGLELSRVTTQQIN DSRWSIIWSVLFGMLVGLIGTCI LVKVLLG/IIFG*TYKSQLEQR QAMGRL

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28613	58981	A	28788	1	1795	MWII SCVMKRTAMNCVLWRK RRRKVCASIFTGKNRANQKRD NVELFDARCRPLNDAADTVRY LPVLT VQLLDKQRLTVLKKIL FGLEPYEISTLFEQRQAMLQSIK EGVVA VDDRGEVTLINDAAQE LLNYRKSQDDEKLSTLSHSWSQ VVDVSEVLRDGT PRRDEEITIK\ DRLLLITTV PVR SNGV IIGAISTF RDKTEVRKLMQRLDGLVN YA DALRERSHEFMNKLHVILGLLH LKS YKQLEDYILKTANNYQEEI GSLLGKIKSPVIAGFLISKINRA TDLGHTLILNSESQLPDSGTAA CGQSLNVLYQRIVGERKLHITGS LMSAAGKSNPLAISGLVVLT LI WSYSWIFMKQVTSYIGAFDFTA LRCIFGALVLFIVLLLRGRGMRP TPFKYTLAIAL LQTCGMVGLAQ WALVSGGAGKVAILS YTMPFW VVIFAALFLGERLR RGQYFAILI AAF GICTATQRNRLLPCKNQPC KANQYQGTGDVLNQLHIDFRA FSGVMVAGSRQIFANEISSGAS NVGVVIFSTQDSANTFNVLNAS GGRSVYPVMSDDMNGSSWK F STRMQKIDPALSVTSGQLMSHIV
28614	58982	A	28789	190	2058	
28615	58983	A	28790	199	293	RYPPAETELS*RLCRLLR*STTV RL*LCRPL
28616	58984	A	28791	685	1557	
28617	58985	A	28792	1	2850	
28618	58986	A	28793	265	535	RIATIRHPSCLHRVGDQYDSLFR TATTQRHCRRMHMMTIGYQFQ PGALVR*SRANHFPGRGDVNI.S SRYSNAPGRRHQHQMRRGFVA RSQ
28619	58987	A	28794	409	1305	

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28620	58988	A	28795	379	1703	LKTVLV DGVVKA EKLVEGAKA VLRQAINGDL DWKAKRQPKLE PLKLSKIEATMSFTIAKGMVAQ TAGKHYPAPITAVKTIEAAARF GREEALNLENKSFVPLAHTNEA RALVGIFLNDQYVKGKAKKLT KDVETPKQAAVLGAGIMGGGI AYQSAWKGVVVMKDINDKSL TLGMTEAAKLLNKQLERGKID GLKLAGVISTIHPTLDYAGFDR VDIVVEAVVENPKVKKYPSAG VFHQLYCRDVVIPMFAIYTFGP QIVGLLGLGVGKNAALGNVVIS LFFMLGCIPPMLWLNTAGRRPL LIGSFAMMTLALALLGLIPDMG IWLVMFAFVYAFFSGGPGNG FNRVKEEFDHERFLVALTNYGT AMCAFEDAARYAN/LARAVWR GYWSFPVDSGKIRPHGDQIKLH EKHAV*SSVESRQRHHHLWRC SDVQILLRQCGI
28621	58989	A	28796	713	902	CRLARPSPLKRCFCSTTHSCI PPPLAATRWPVRRRWRPSMCC WSRTYR\PG*AKRRYTSPA
28622	58990	B	28797	1	1521	
28623	58991	A	28798	348	599	RHFQRLSRSSDSNP*LDPTLFA SALASRQRVTESWSEHPDPLQ VRRKTEDVKTTPPFLQSAHRS VNIVLWIRGFSPDLLV
28624	58992	A	28799	582	732	
28625	58993	A	28800	1	1443	
28626	58994	A	28801	1051	1173	PETYRRIAGRYGATCGTLR*RA SGG*TGETDAAGPGYPPAR
28627	58995	A	28802	1	2742	
28628	58996	A	28803	435	1143	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDHK RPREALLDSLKKLQLDYIDL LHWPVPAIDHYVEAWKGMIEL QKEGLIKSIGVCNFQIHHLQRLI DETVTPVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQQ GKGVFDQKVIRDLADKYGKTP AQIVIRWHLDSGLVVIPKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGGKRLGPDQFGG
28629	58997	A	28804	1040	1079	
28630	58998	A	28805	300	567	SAGFKKSGTRHCDVRPGACGT TLYQRR*VH*\WSTVHKPETSS SKMHGQRGSGLLAKSLVANVI CSLIRNPLPIMPPLCAFVSLKM IKKRPRRH

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28631	58999	A	28806	167	327	KNNSSISGINATER*KTDENNTS VFSSPGKFYRTRTAPLTD RRTN SPAYLSEL
28632	59000	A	28807	1	1197	
28633	59001	A	28808	1	4104	
28634	59002	A	28809	1	1368	
28635	59003	A	28810	82	1143	
28636	59004	A	28811	72	212	
28637	59005	A	28812	1	1078	MKDVTLVLRPQDAGANTCAHIL SQLPHLQLPTLETGLINALGY APGDMQPSDSATWGV AELQHE GGDTFMGHQEILGTRPLPPLRM PFRDVIDRVEQALVSAGWQVE RRGDDLQFLWVNQAVAIGDNL EADLGQVYNITANLSVISFDDAI KIGRIVREQVQVGRVITFGLLT DSQRILDAAESKEGRFIGINAPR SGAYDNGFQVVHMGYGVDEK VQVPQKLYEAGVPTVLVAHHQ RVFAIFAVADITQVINIQYCRC QQAACGRRKDQCRNQSKENQY GNITQTDITIRTIAHGVVIAAMI DNPPRIRKPTKSAS*LWWPLFY LLAVSLFTLWNRVRFHGLSAS SSPLRPTY
28638	59006	A	28813	429	611	AAKHPCCGYSFRRRTDVDHNG YSGNACTRLHHAGGIRQ**PNF GYSPPASSCGQVSQNSS
28639	59007	B	28814	1	2703	
28640	59008	A	28815	1931	2407	HGLRTRQRLSKASRICAALLCR LLTYELSSARWMWITTAVCV SSCRRWKKPAALVRPLPPASAP GFITTSAPCCASRNG*KSSFQR TLHVSRRHQSRTS*SPQVDTSDN SSEIVNNQAPTARTGSGLRVAV LEQRVQEPLAANAPPQLRVSAI NAAS
28641	59009	B	28816	430	823	
28642	59010	A	28817	1	2667	
28643	59011	B	28818	204	2659	
28644	59012	A	28819	1	2817	
28645	59013	A	28820	1	1089	
28646	59014	A	28821	1	1891	
28647	59015	A	28822	2972	3318	KYALTLVRFVTLKVQSVTALK A/CGLYRTEFLFMDRDALPTEE RQFAAYKALAEACGSQAVIVR TMDIGGDYELPPYELPERRDPV SSAGALFVSRWIVERSCADKFR VFCCGASGFR

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28648	59016	A	28823	1	1030	MMCIMYRTASSLANQYHIDSE QARRGSQNAFDVNFEAWQLEI NHVLEAASAQSQRNYQISALVF ISMIIVAAIYISSALWWTRKMIV QPLAIIGSHFDSIAAGNLARPIA VYGRNEITAIFASLKTMQQALR GTVSDVRKGSQEMHIGIAEIVA GNNDLSSRTEQQAASLAQTAA SMEQLTATVGQNADNARQALG TGKNAATTAQAAAQFIDRCQ ADFTRGAYRYRSGTYFICQYLT VTVSGIDAHQRGQTDTRILLQ LFLVQFDTHRQTLNDFDPVTGR ILRWKQLDRAAGDITGHRTDN TSTLQRQPGVTYFGGSLLHGW *SSSLVPRIIA*LALYC
28649	59017	A	28824	1	3087	
28650	59018	A	28825	376	1564	
28651	59019	A	28826	1	1174	MVNLALWLKKHRFRLDQVQN FYPSPLANSTTMYYTGNPLAK IGYKSEDFVVPKGDQRRHLK ALLRYHDPANWPLIRQALEAM GKKHLIGSRRDCLVPAPTIEEM REARRQNRNTRPALTKHTPMA TQRQTPATAKKASSTQSRPVNA GAKKRPKAAELQCPLVMTSGN LSGKPPAISNEQALADLQGIAD GFLIHNDRDIVQRMDDSVVRESG EMLRRSRGFLPTGRGLRIDYKQ KMRGTRRAGCNFNQSGQGRPS LKRGEQTDIKKAKKQATGLAG ESMLQDDAFYAVITHAAGPQG ALPLTPQMLMESPSATCSA*RR TPGWAGTPTSSPAKRC*LSALRI TSSGSTPSCSRRHWRKRARRSD ACHHSRFSPTVWPVTQPKKGR
28652	59020	A	28827	1	1392	
28653	59021	A	28828	1050	1154	
28654	59022	A	28829	1	2649	
28655	59023	A	28830	59	511	
28656	59024	A	28831	1	2421	
28657	59025	A	28832	4594	4770	PSTSTIHAYVSGKSRISPHTREA MI\NDHSKRAWLYALRRRAGR TRHRCPGRTGRQRL
28658	59026	A	28833	1	727	
28659	59027	A	28834	1	3069	
28660	59028	A	28835	1521	1841	FLPKSLGDSSGESRKHRRRRRA FSPDQHPAGNYRTRLSARPFV* RCLYYSR*ARRGNYRQH*TTSP ALYQAASPFQ*SIAG*RAGKTR YRSSVYLCVDHFDHSGSW

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28661	59029	A	28836	1	1644	
28662	59030	A	28837	1	1245	
28663	59031	A	28838	1	1518	
28664	59032	A	28839	3	491	
28665	59033	A	28840	1092	2827	
28666	59034	A	28841	162	1760	
28667	59035	B	28842	1	3378	
28668	59036	A	28843	434	763	
28669	59037	A	28844	1	3066	
28670	59038	A	28845	576	783	PGNVLRLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFAC ETRMYPEEPVYLPPRYRGSIVIH SIAF
28671	59039	A	28846	855	1134	PGNVLRLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFACR ETRMYPEEPVYLPPRYRGRIVL TRDPDGEERCVCACNLCAVAWP VGCISLVS
28672	59040	A	28847	1	890	
28673	59041	A	28848	420	943	CLAADALHLRCLINARHNAQQ EDALVEKAKQ/VTWRLLAAGV CLLTVSS/VARADSLDEQRSRY AQI/KQAWDNRMQMDV/VFIHAM PTNTARPTASSTGNIHLVSVLA GAPARWSACWDHCNDQIAPCR ELSRLLRLHAQYQNTKRVHT QFSGYKTPEMANTAVPTISSQR RALFNPH
28674	59042	A	28849	1	1247	
28675	59043	A	28850	533	1029	SKSIMLLCRSVVSMIRRTVAA FTLAAISVARSVLNLIRDIGM QAMPLCRSTTGRNRWTSSAKR TILR*RQRILPLTPC*HRMFRSFL KKILSDGKSVTLGALLADVTQS DEPL*GSPAGS/TGQMPAIQPAQ KTHHVKAHSFCS*PAQSSPVNP DDIISFSKSK
28676	59044	A	28851	749	1050	SPHMPGITAGTSPFSVPLAISAPSI SAKSLPGKTA*AWPNIMALTPG ISLR**TEFSAITLYGSADSPECA RTT/INIGTFLAHRHVFAHGF NIIHRHFG
28677	59045	A	28852	260	717	RQLRTELSAGIAAFRTGNAPAIL RFMKLAPPP*WRRKPLTGV*RV *RGRDSVR*VAFVPTVSIAIQL DPRSLLQQDAFKKAGLDPEQPP KT/WQDLA/VLCRETESLRHEV RLRQRLAGLDPTGKL*AWNGM MPYDADAKDAPQKPLSAEPAC
28678	59046	A	28853	776	2730	



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28679	59047	A	28854	383	1367	RPTCWTSIEWVRRVRTAALRSS GKTWVFCCRRRIAGELMLTNR HTGGVMVTTFRASEAFAGALE LTGKATLVALINRCIGAVIRYM LIAVIPDIFQRLQVVLNVWILAV ANETTQRQRRVRRFKVDLVVR VHLLLHIEVETVGVVTFIGHAR HHAKLSSIETAEIAQVFTRRA VETETITRFFFPLIHCLTQTFNN GDTFRAKLLVVVNMLAAEQRV NGFVDADVTQRNRRTTVFEDF RNIIVSIETHATSTRYG*CVGPP AMRACSGAVQPQWLHPGKL RQGEPSRDLVRQRPAAALCLPRR HRILRGYNGNIQRRLYSTGNGL
28680	59048	A	28855	1	1477	
28681	59049	A	28856	1	793	
28682	59050	A	28857	1	1020	
28683	59051	A	28858	1	613	SAGDGARIEQFDRKGMVNNKF NYFIMSKLAEAGIPTQMERLL\AS DTECLVKKLDMVPVECVVRNR AAGSLVKRLGIEEG\ELNPPLF DLFLKNDAMHDPMVNE\SYCE TFGWVSKENLARMKELTYKAN DVLKKLFDDAGLILVDFKLEFG PVQGEVVLGDEF/SPDGSRLWA QETLEKMDKDGFRQSL\GGLIG AYEAVARRLGYT
28684	59052	A	28859	1	1002	
28685	59053	A	28860	1	422	
28686	59054	A	28861	625	750	RNVQALQGAHGTGGALTDPA* QHLGTLCADLL*NGLSPSPRD
28687	59055	A	28862	1	1449	
28688	59056	A	28863	105	297	
28689	59057	A	28864	55	423	DRPQRNRATLMQLYSRGSPIR RLEHRFEKVQGKPGFEVFIPGF KQKGLGRPLGVKALVFGIDTGL FQLQAVKNLDGF*FDEASASQP GSDNILRELVRATGRADGSGT GFTEDANSFTSYR
28690	59058	A	28865	1	2340	
28691	59059	A	28866	314	696	

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28692	59060	A	28867	458	2160	PTLRAFYRVTPHRSLSVMLALK CHGINPLRSWVG*VE*EEKY NMQT*/E/LENWKPISNLHDMSS SHSKTLGYKRLTKSNPISCQILL YKSRSKGRKNQRSTRTHCHHPS PKIYSASAKEPWILATNLPVEIR TPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDI MLLIALMLQLTCWLAGVHAQK QGWDKHFQANTVRNRNVLST VRLGMEVLRHSGYTITREDSLV AATLLTQNLFTHEEAPANSVPA AAVIRRVQALIGITGRKAHAGG SWNGTASSDNFPNIFILPQNDP MALAAAVAPPELEALLAAGKV SVKIQEPCDEILFSRAKVWNGE KWACVTIVGGHTNIVHIETHDG VVFTQQACVAEGEQESPLTVLS RTTLAEILKFVNEVPFAAIRFIL DSAKLNCALSQEGLSGKWGLH IGATLEKQCERGLLAKDLSSSIV IRTSAADARMGGATLPAMSNS GSGNQGIGTELNVSCRFPATNL FVHDPTQQAMQRNQRRAVQT FPVWRVAQHCAVRPFRQRIQQ LRDIFHLKGDQFTNRPAKIVAF
28693	59061	A	28868	2095	2722	
28694	59062	A	28869	789	2509	
28695	59063	A	28870	57	440	CSWDPQDPHGILQGAGKEDSQ AQKTTARQKRKTRKTATRQKK HEKQSEESTNEDT*ARKVEETQ HKHDAESTSGSVIQCVCVQLFTQ SFTATPAASATTATRPILCSSR ARAGYPSTTGVSRRRESPL
28696	59064	A	28871	3057	3495	MPVRGQRPVSLARHPGTRSDK KGHFVVAHPAF/P/DQFLHAAM DIKQPVISIDNLLAIHKQAEVTR FIGGDMQRRADRDHPRIAAVALID KRIRFGISRRFRAQSIHRIFAQR MHIFRPVIGQHQAATGNSRLSAS TQRLHHNPAAFFGPFH
28697	59065	A	28872	1609	2112	HQPVLTVVMVPVSPLIIRADNP FRDEVGFLCQPAVTVIPVKIVR VTGDTVIRPHAEGAVRVQLRV GQAVTCRVCGIRDADIQIRCGG VNAGQPAGGAVAVTPGLARAA DADEFVAVVPGVIAVRQQAVQ VLAL*LPGRGISGGEFITA EVRS VSRCSRVSRYSTRGIL
28698	59066	A	28873	2	712	
28699	59067	A	28874	337	383	

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28700	59068	A	28875	65	436	REVWEHAKRMLGDSSSLDMGM DDELTVMVAYEYIGRLGKTATI HWKVKSSPSMVWSASVWKKM ALR*LSRTLRLPNQEHSL*ASVP ELKCAASWTKRKKNSTFIASSA IRLTLTWKPKPFLSRL
28701	59069	A	28876	206	403	
28702	59070	B	28877	1	2046	
28703	59071	A	28878	1	1335	
28704	59072	A	28879	1	974	MEAPPIEDVSSRDNLNRRRNYGH PADLFWFYSLRALPEVYASSD AHEKFVKDFVAAWSLNLVLYQR IVGERKLHTGSLMSAAGKSNPL AISGLVVLTLIWSYSWIFMKQV TSYIGAFDFTALRCIFGALVLF VLLLRGRGMRPTPFKYTLAIAL LQTCGMVGLAQWALVSGGAG KVAILSYTMPFWVVFALFLG ERLRRGQYFALIAAFGLFLVLQ PWQLDFSSMKSAMLAILSGVS WGASAIKRLYARHPRVDLL\ SLTS\WQMHVCRQLASQLPLSH GAMPRCRRPGHSSNPDRLANVI ARRVLRGMSNRQVPSPCCP
28705	59073	A	28880	1789	2026	CRFFWIN*YCNVSFGANLERA* TSFSALFIDLQPPGYRTTTSKHK VSSSLIKGHVLLDHSFHDNTQ LWISTNAFRFGN
28706	59074	A	28881	568	717	
28707	59075	A	28882	1760	3092	
28708	59076	A	28883	1	1206	
28709	59077	A	28884	1	575	MSGYSYSSVWAEDDIQFDSRFLE LKGDTKIDLKRFSSQGYVEPGK YNLQVQLNKQPLAEEYDIYWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSHDGKCLKP GQLEGVEIKADLSQSALVISLPQ AYLEYTWPDWDPSPSRWDDGIS GIIADYSITAQTQHAKLNTEDD/ SNESTGSVWQGLWRLQDD
28710	59078	A	28885	1	718	
28711	59079	A	28886	1326	1953	PARSPEAEAAAACFRSWEWSR YYAWRALPSLKAKLALGEDY LNSDIFDGFNYVGGSVSTDDQ MLPPNLRGYAPDISGVAHTTAK VTVSQMGRVIYETQVPAGPFRI QDLGDSVSGTLHIRIEEQNGQV QEYDISTASMPYLTRPGQVRYK IMMGRPQEWGHHVEGGFFSGA EASWGIANGWSLYGGALGDEN YQSAALGVGRDLSTFEA

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28712	59080	A	28887	491	681	PTGHRAQKKWNT*TRHSNSY* KNFAKKLI*GDIREKLQKLEGF AGMNATQLIEVATEVYINCDQE AKKETEQRRLRKKANLLAAALT KRKINIVKGRECSHGCGHGRGQ VEQRAKRWLRLRGGWVKAFF VRTEKAREVTKVLLRDIHPGFGL PLTLASDNPAFIAKIVQELTQL LKIKWKLHIAIYWPQSSEKVEH MNQTLKQLLKKFCQETHLRWD QVLPMLVLLRVRYTPTKQTGYS PMRSCSANLK
28713	59081	A	28888	1	963	
28714	59082	A	28889	123	593	KRQVLAGFLITPRRLPKNWT WCWWSM/PAQVKQVLFGETG VAQHLKPGTAVMVSTIASAD AQEIATAGFDLEMLDAPVSG GAVKAANGEMTVMASGSDIAF ERLAPVLEAVAGKVYRIGAEPG QVRP*KLFTSC*RAYILLPEPKR WHLQPVR
28715	59083	A	28890	263	467	
28716	59084	A	28891	1218	1505	AGGDAANRRRLIQHVCSLPLYT GLPRGPHGRAAGNPVDQQFAA GDLGLSPHADAHPGGTDDVRW CLIST*KRWDSGV*AGAGQYSG WRRRSLRWR
28717	59085	B	28892	1	2118	
28718	59086	A	28893	1084	8334	
28719	59087	A	28894	2029	3313	
28720	59088	A	28895	1168	1236	
28721	59089	A	28896	1	284	
28722	59090	A	28897	1	1188	
28723	59091	C	28898	20	878	
28724	59092	A	28899	1904	2281	CSAYAGLHPFWLKSTRFCTHIL APATAISPNTTIDAPPITAAGMV *ISAPNFGEKPNSMAMTAAATN TSVE*TLVTAITPIFSA*VVTPLP PTEPESIVARPSPTNARPIYGSIL RPVIPATALR

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28725	59093	A	28900	773	6228	MKARLHLLYPMGLRAWCGPV RLCWNLISLGLWSCFSKGWVT TPTTLSCSPPPRRGRMAPWAW GRSRARMCWSWSWSTRPSRPC AVRWSWSSGATGSCWRRPVST APPRPPPWRPAAPTAPLWART RMPSHWPSTTAPAATAY*/DPD AGYQPTPLAAPAEPGSKYSLAS LDRGQGRGGGGGGGALEYVPKA VSQPRRHSRPVPSGKYVVDNSR PPTDLEYDPLSNYSARHLSRAS SRDERAAKRPRGSRGSEPYT
28726	59094	A	28901	1116	1497	RGLISDLPSKPSCLMWAASCRN PASLLASE*TVSNA*IPAERAAC KMEQRANSSSVPSGERSVRRLR T*SSAPRAIPKRSEA*AISTARVI PSGDSIAASRPVLPGRPQAFSIR RISFSISRTS
28727	59095	A	28902	1	2916	
28728	59096	A	28903	1	2001	
28729	59097	A	28904	179	324	
28730	59098	A	28905	1591	1806	
28731	59099	A	28906	531	949	
28732	59100	A	28907	44	477	
28733	59101	A	28908	161	333	
28734	59102	A	28909	1	394	MEGVAFLTFLAARA AVGNRPA SPQIVRKQREGHGILTRDPVA FDDVAVNFTQEEWALLDISQR KLYKEVMLETfKNLTSVGKSW KDQNI EYEQNPRNFRSLIEK KVNEIKDDSHCGETFTQVPDDR LNFQEKKASPEVKSCDSFVCAE VGIGNSSFNMSIRGDTGHKAYE YQEYGP KPYKCQPKNKKA FR YRPSIRTQERDHTGEKPYACKV CGKTFIFHSSIRRHMN SHWEKP YECSKCDKAFHSSSSYH
28735	59103	B	28910	1	534	
28736	59104	A	28911	238	434	LPCKIHTPNHGPLKNIPSTKN*Q RRRNTSQR*LRHQPFSSASRPG SRLRFAIGPLQPAEAGMVT
28737	59105	A	28912	358	878	KLCHIACIHSVSFQCESFHVFTG FLSSVCPFMKSKIFDRSEGF PKL LTLIGVLSSVSPFMISKGSEGNK GFPTLLTLIGFLSSVRFFMYLK* LGRIKAPPTYLT FIRSLYRVHYV CLCPFMNSKVLGRSEGFPTFLT CIGLLSIVCRFPTLLTLIGFLSSV SPYMISKGTGMR
28738	59106	A	28913	1382	1416	

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28739	59107	A	28914	1	333	MFQDPVAFDDVAVNFTQEEWA LLDISQRKLYKEVMLETFRNLT SVGKSWKDQNIIEYEQNPRRN FRSLIEKKVNEIKDDSHCGETFT QVPDDRLLNFQEKKASPEIKSCD SFVCGEVGLGNSSFNMNIRGDI GHKAYEYQEYGPCKCQCPK KAFRYHPSFRTPQRDHTGEKPY ACKECGKTFISHSSIQRHVVMH SGDGPYKCKFCGKAFHCLSLYL IHERIHTGEKPYECKQCGKSFSY SATLRIHERHTTGEKPYECQQC GKAFHSPRCYRRHERIHTGEKA YQCKECKGAFTCPQYVRIHERT HSRKKPYECTQCGKAL*YSLKS GSLMP*ALFFWLRIVLAMWAL LWFHMFNKVVFNSVKKVIGS LMGMAWNLQITLGSMAIFMILI LPIHEHGMFFHLFVSSLISLSSGL
28740	59108	A	28915	1619	2353	
28741	59109	A	28916	1	1252	MSYSVMFALLLTPLLFSLLCF ACRKRRLSATRTVTVLHSLGIT LLLILALWVVQTAADAGEIFAA GLWLHIDGLGGLFLAILGVIGFL TGIYSIGYMRHEVAHGEISPVT LCDYYGFFHLFLFTMLLVVTSN NLIVMWAAIEATTLSSAFLVGI YGQRSSLEAAWKYIIICTVGVA FGLFGTVLVYANAASVCGTDH GGRMMRSWNGGQLISKLLAIT PDKLVLDGFSQAEDNIAVLKA QHISIS/AETQGAKVEFTVDQLQ QSEYLQLPAFITVPPPTLWFVQR RRYFRISAPLHPPYFCQTKLAD NSTLRFRLYDLSLGGMGALLET AKPAELQEGMRFAQIEVNMGGQ WGVFHFDAQLISISERKVIDGK NETIPTRLSFRFLNVSPVERQ LQRJIFSLEREAREKADKVRD
28742	59110	A	28917	2	2282	
28743	59111	A	28918	518	1046	
28744	59112	A	28919	8	893	
28745	59113	B	28920	1	3129	
28746	59114	A	28921	1	1284	

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28747	59115	A	28922	3612	5412	PGLKHQNNNGHRGPDAETKGV RDFGPNKPLAG/VRLN/LERLR DTHHIDVAPLVARLDQMMESV SQLQLARAGQSFSSGNYQH KLEDVILPSYDELSTMLDQRQ QTLLLPEAADITVQGDATILR MLLRNLVENAHRYSPQGSNIMI KLQEDDGAVMAVEDEGPGIDE SKCGELSKAFVRMDSRYGGIGL GLSIVSRITQLHHGQFFLQNRQE TSGTRAWVRLKKDQGAYPMSE KVVFSQLSRKFIDENDATPAEA QQVVYYSLAIGHHLGVIDCLEA ALTCPWDEYLAWIATLEAGSE ARRKMEGVPKYGEIVIDINHVP MLANAFDKARAAQTSQQQEW STMLLSMLHDHQAENAIYLMG VFIMLIFFPAPVASEKPLSPDCW TTHTLRMIGENSGLVSYMREK AVSPNCWNVIHYSGLHLLELLS SYDVDVNQIINTICEWISLIKTR GVRPEFQTLLTGSGSEHGERFI MNRPTLFFTDLAFHVDRTQYV HDTAQSRTYRDFNRVFEVFI QTATQTVGGTHCDAPGWFWF GAVQSVPAALIAVAAAPGLA SFLPFARRVPRTVVALLAQAAA YADGMPARADGSFNSP
28748	59116	A	28923	1	2910	
28749	59117	A	28924	470	723	PGFGDARKKLISLNFFIWV*TA*I M*P/LAGSDFVYRNS*RNVFIAQ TLQLRSRQPVTMHHATRAFT EHNILIRFECCEYSRYLFT
28750	59118	A	28925	599	1117	
28751	59119	A	28926	279	455	SLSHSSGRCSRGGISFWVWVEF GPVACLAASVV*L*VSVVWLW LSPSGQGCLGCRVWL
28752	59120	A	28927	1	2913	
28753	59121	A	28928	1	2328	
28754	59122	B	28929	55	327	
28755	59123	A	28930	9	107	
28756	59124	A	28931	1	2106	
28757	59125	A	28932	1	1123	
28758	59126	A	28933	260	709	
28759	59127	A	28934	467	631	LEVIEAPQPNWS*SVQQSACST WPGCWVDLEDQVWVWYEW TTKRASLLPIFQD*LKALRKAQ VWAFAS*STWPGCWVDLEDQV VWVWYEWTTKRASLLPIFQD
28760	59128	A	28935	989	3010	

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28761	59129	A	28936	3	183	GLYAKSFAQTLYLEQRLAVLR AYFYCALWNHSVSVVAG*CKT DDSANAGDGGSGADRSR
28762	59130	A	28937	1	1006	
28763	59131	A	28938	185	384	
28764	59132	A	28939	2	615	WAFRVIRFIVTANWSLKAVWM RRLIVVAALLTLRTVPMRQLNR LLLITPSLSRHMVSTGPATSCVN RGFLSPTVVSVLSGSPFC/WQDG DQTLTFKVDYIATGKATSEGEE QISLGVRNTSPDVPYLIQSWVM TPDNKKSADFIITPPVFVLNPGN ENLLRIMYIGAPLAKDRETLFFT NVRAPVSTTKRKEGNTLKIAHK RMITN
28765	59133	A	28940	1	1686	
28766	59134	A	28941	76	981	
28767	59135	A	28942	1	1998	
28768	59136	A	28943	300	506	DLYWSLNSGKQIQSGRIDDRSA KTVAPHAPHRQWSASYWRS *SSSFRLNKKCHTQNHSCIKM ARE



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28769	59137	A	28944	1	2539	MPIEEPALRSWQRPFLKWAGG KYSLLPELDRLLPAGKRLIEPFV GGGSVFLNSDKHERFLLADVSA DLINLYQMLAVVPDSVIYEAM KAFRHLNDAENYTLIREAFNAQ RLDAVERAAFLYLNRHCFNG LIRYNLDVFFNVGFGKHKQMT NNEKGPFEGLLVIDMTHVLNG PFGTQLLCNMGARVIKVEPPGH GDDTRTFGPYVDGQSLYYSFN HGKESVVLDLKNDHDKSFGHT GPLKDAPAYDTIIQAMSGIMME TGYPDAPPVRVGTSLADLCGG VYLFSGIVSALYGREKSQRGAH VDIAMFDATLSFLEHGLMAYIA TGKSPQRLGNRHPYMAPFDVF NTQDKPITICCGNDKLFSALCQ ALELTEL VNDPRFSSNILRVQN QAILKQYIERTLKTQAAEVWFT PFSNKYNGHRIARTDKASMPTV YSESLFVEGIIRASTSMTTKQGP SLRTGRTLRLKFCPLSETAATTDS SIFPSKFTPTASRLPGFSFIRSPK MTQSVLLPPGPFTRRQAQFTT TYSNITLEDQDQSHFRLVVRDT EGRMASVQTRPPADREAFTRIH LPEHTLYPHTPAIAAGVFIDGDI PMTTQTQHDLPANQPEFELTV TPVPDEQRIDFWPQYFGAIPQW LLEPHIFAWMDRFCEGYSGGI WSFYTLNNGGAFMSPEPDNDT WRLFNCLNATMPYPYRMTCGTV
28770	59138	A	28945	907	1917	
28771	59139	A	28946	1	3033	MVWGFTCSTTATLEGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQDTLTQMMTSTLFSSPSV HNVMETVTQETAPPDEMTTSTFP SSVTNTLMMTSKTITMTTSTD TLGNTTEETSTAGTESSTPVTSV SITAGQEGQSRTTSWRTSIQDTS ASSQNHWTRSTQTTRESQTSTL THRTTSTPSFSPSVHNVGTVSQ KTSPSGETATSSLCSVTNTSMM TSEKITVTTSTGSTLGNPGETSS VPVTGSLMP
28772	59140	A	28947	636	725	
28773	59141	A	28948	1	1123	
28774	59142	A	28949	2345	3644	

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28775	59143	A	28950	34	437	CGRLLQKSGFVVSVIDGIERL NTRRARGLPNGTACGQQFSSFR GAFCTQVAHIVFCTEGDTDQ/D ARKRERFPLRG*SPAIEQSPPAG RCCRVHDHRLFRYAGSFFQYPE HPERYRFSADAQRPHHRERRLP
28776	59144	A	28951	1	457	
28777	59145	A	28952	176	757	KPMKSTAAAADAALLSAIERQ VIDDAAAHLSEVAQGDDVDAL EQAICKNVKQTDQFAARRMDQ SVRRADRSDLIETFDHVCTVIFI RDGITSAEVETADTARGNVVDVI RTGEVGAVCGTEETKSILQYLQ YAITKDIFATLCVLLQDGKNNV LLTHTSQVFQPHIFAESDQLRN RRIFGDRFDSPPVSIRMMFGL
28778	59146	A	28953	1	1503	
28779	59147	A	28954	425	619	AGWSFLPSPAEQNRWRFPPLSRF CQIPAPLQVRS*LACRFFAAYSP PLLRKSPAASMAAYTTSRLH
28780	59148	A	28955	55	476	SYHALANVFYQRRMAITQVAG RQAQVFKAHLRDDVHHHIDGQ VTATESVMEGNRHAVL*TRAT NRFFQVGAQFAIARFFSLVGLL WRVLESGKIAFSATIPGRYPFLS LRLFNFLRHFDCILIRGCRKVL HGRAPDGRDR
28781	59149	A	28956	92	3254	
28782	59150	B	28957	12	271	
28783	59151	A	28958	309	1238	GSGSCYSALVKKWSARSLRA DRNGARRGAYVGRKFGHFGPG LAGFFSAHASNLCRRSDRAHAH YHQLLNFAADPVDMMQ*KRGM VFLLLMDQRQQRVDDWRRLPS LLSVWQSCGDSGRRAPGGR*FH WRFQATVFQALAEGLRRNLQI VVATVAF/GMGINKPNVRFVVH FD/IPRNIESYYQETGRAGR/DGL PAEAMLFYDPADMA/WLRRCL EEKPQGGQLQD/IERHKLNAMGA FAEAQT/CRRLVLLNYFGEGRQ EP/CGNCDICLDPPKQYDG/STD AQIALSTIGRVNQR/FGMGYVV EVIRVAAPLEPDYSHRP
28784	59152	B	28959	1	2123	
28785	59153	A	28960	1	2834	
28786	59154	A	28961	1	2505	
28787	59155	B	28962	145	494	

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28788	59156	A	28963	1019	1329	ISGVFFACFTNGSNG*LAHCHA F*PLLGDGFCRNGVIQGRENAH LMNGGGRRVTALHFQQYRFHH LFNILTARHHLIDNANHAQIDR* RFAFMRLAGGTATHQ
28789	59157	A	28964	1	1423	
28790	59158	A	28965	1	863	
28791	59159	A	28966	1	2412	
28792	59160	A	28967	3066	3155	
28793	59161	A	28968	1	1215	
28794	59162	A	28969	1	1678	
28795	59163	A	28970	1	4674	
28796	59164	A	28971	1	393	
28797	59165	A	28972	2026	2703	NSRCVWNAEFGHQLIAGDHFF HHFQAHLVQFGGDFQFLNLG EGQLVVSIFTPVRLAVHGVKIE TVFVGFSSLIHGSQTVLVSSASG ASVASTRGKCTIVTSGISG/VIA KND/GLPRVHGATAPSCASQFL VFAAPTTPRDRHG*RTDDSTPQ RLSSPAVEKAPTASSASGNSRN DKPLREITLITSDRPVPDAAVSP TGFWPLTIPFHRCRRMSSLPGIPI RQSSA
28798	59166	A	28973	475	661	AYGNPVEYSRRAPGGR*FWH RFHGHGFPGAGGGSPAKPVNR RAAAPIDSAPAPAADGRVSR
28799	59167	A	28974	367	1464	
28800	59168	A	28975	904	1473	
28801	59169	A	28976	738	893	
28802	59170	A	28977	1	1108	MADTRYFGMHMSQETPASTTE AQIKNERRISPFWLLPFIALMIA SWLIWDSYQDRGNTVTIDFMS ADGIVPGRTPVRYQGVEVGT QDISLSDDLKIEVKVSIKSDMK DALREETQFWLVTPKASLAGV SGLDALVGGNYIGMMPGKGKE QDHFVALDTQPKYRLDNGDLM IHLQAPDLGSLNSGSLVYFRKIP VGKVYDYAINPNKQGVIDVLI ERRFTDLVKKGSRFVNVSGVD ANVSISGAKVKLESAA
28803	59171	A	28978	1	861	
28804	59172	A	28979	5	337	
28805	59173	A	28980	1	612	
28806	59174	A	28981	128	1742	
28807	59175	A	28982	1	2688	

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28808	59176	A	28983	361	738	FLQPFPFKREINKFIRDIANNMK TDFSAVTLFTDCVTVMWLWII*F FQRKFFLKGFIPPLGSFYRE*IIT SLFLYLLCNIFLATHRISCDDFSF NIQHVKKFWDSNLRFLIRLDL SDDQTVHC
28809	59177	B	28984	1	1263	
28810	59178	A	28985	363	569	KGYSRRSGKHRQGCCNVLRRLR FPDHQTAPRPMPLKRQTRAPGQ SPPGLPADPHPGQF*LPLLGRGRF AR
28811	59179	A	28986	1	1035	
28812	59180	A	28987	275	721	LMVSGFLTSPKDERIMSGEAR AILIASNSSVLVCAFRNFNKSFT DLLPSELAQSASERISFNNTLKD SGMPGSI*WLPSTMFLYILVRPF TSSDLTVSISCRVYAAPYASSA HTSISPKR*PPNTQRLLTGPVGT FWGRKPPLFPTP
28813	59181	B	28988	1	2082	
28814	59182	A	28989	1	1567	
28815	59183	A	28990	1	453	
28816	59184	A	28991	1	777	
28817	59185	A	28992	1	1431	
28818	59186	A	28993	1	561	VDSRGYPYGSRGAGKCRESERL GSESRNPGSIGLENELTAEDVAS ADMVILTKDIGIKFEERFAGKTI VRVNISDAEFLMTNRISRLKTA LFANTREISLERALLYTASHRQT EGEPVILRRAKATAYILEHVEISI RDEELIAGNRTV/ITARRDYVA GNGPLLAERAGSIPDASAGPL CYQRRRL
28819	59187	B	28994	1	3414	
28820	59188	A	28995	1082	1297	MIMWLA AVAIREINHDSGSATF RTPRDPRTVAGKYNLGASLYK SELLA*LHSAGAGCLSCQRAKL GLGRRR
28821	59189	A	28996	1	2115	
28822	59190	A	28997	168	317	
28823	59191	A	28998	1331	1471	RWSNGTLENGTL*LLTLPSASLI STNKSPLDDVE*RSLISKAPGDT
28824	59192	A	28999	147	1456	
28825	59193	A	29000	1	439	

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28826	59194	A	29001	722	2805	TPRAERTASSVALPTSRLRLAR AETTTAPSTPMKTHRVISMVFF TCSQTGTPSASPVKSSLKVSSLN IIIASTTNRPS/VQQF/WPVSPPG DGTRRYP\SISLTVLTGNDNVNL LRAGIDLAIYFDDAPSAQLTHH FLMDEEILPVCSPEYAQRHALT DTVINLCHCTLLHDRQAWSND SGTDEWHSWAQHYAVNLPTSS GIGFDRSDLA VIAAMNHIGVAM GRKRLVQKRLASGVYPPRCAY PRTHLLETSTTSGVNGVGTYS PFWRMLLSNFVMAFSITLGKIT VSMLSFAIVWFRFPLRNLFFW MIFITLMLPVEVRIFPTVEVIAN LQMLDSYAGLTPLMASATAT FLFRQFFMTLPDELVEAARIDG ASPMRFFCDIVFPLSKTNLAALF VITFIYGWNQYLWPLLIITDVL GTTVAGIKGMIATGEGTTEWNS VMVAMLLTLIPPVVIVLVMQR AFVRGLVDNPAANYIHYGVRE SGMTA IANGIAHHGGFVPYTAT FLMFVEYARNAARMAALMKA RQIMVYTHDSIGLGEDGPTHQA VEQLASRLRTPNFSTWRPCDQV EAAVGWKLAVRHNGPTALIL SRQNLAQVERTPDQVKEIARGG YVLKDSGGKPDIIATGSEMEI TLQAAEKLAGEGRNVRVVSLP STDIFDAQDEEYRESVLP SNVA ARVAVEAGIADYWKYVG
28827	59195	A	29002	2253	2546	
28828	59196	A	29003	279	629	NGAGHL*RPPVDGATAAPAGG RYAHLRVCPESLPWLHLPWRI YRSGS*SAPCHCRNHRSGSAWQ KHYGNRFRFRTVRPYRGRALH LRGRNTAITQAADWRLATAQL LEIAGVGDE
28829	59197	A	29004	313	638	RWRQRWFWCLHCLVLFRTIPR TFALSQCRPWDDSRSDTSMH SIQWNRMYCNCMQDEQEADE ANGKGPAQVGDRQAWAGR/CR SHRREGTIPGNPHPRAS*RAGW QR
28830	59198	A	29005	1	1182	

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28831	59199	A	29006	1	535	RPYVLP\VAGSNALGA\LG YVES ALEIAQQCEGAVNISSVVVASG SAGTHAGLAVGLEHLMPESELI GVTVSRSVADQLPKVVNLQQA IAKELELTASAEILLWDDYFAP GYGVPNDEGMEAVKLLARLEG ILLDPVYTGKAMAGLIDGISQK RFKDEGPILFIHTGGAPALFAYH PHV
28832	59200	A	29007	1	1953	
28833	59201	A	29008	1	656	MKLMAIQEQARGEQCFRDSEW DLQFHIQVALATQNSALAAIVE KMWTQRSHNPYWKKLHEHIDS RTVDNWCDHDHDKILKALIRKD PHAAKLAMWQHLENTKIMLFN ETSDDFEFNADRYLFAENPVAI AKELELTASAEILLWDDYFAPG YGVNDEGMEAVKLLPRLEGIL LDPVYTGKAMRGLIDGISQKRF KDEGPILFIHTGGAPALFAYHP HV
28834	59202	A	29009	1172	1371	
28835	59203	A	29010	338	528	RHPRCDPYGFCPFTADADDA** LGACHHYWRGQRKIYAGSGDS RCQPDGRRSAPARRPLRRQR
28836	59204	A	29011	413	2798	
28837	59205	A	29012	48	320	LCRPDKAFTPHPA*TKRILSAI*P SSFKEGIDHSATFFFAARFALVA AAIFCVFADGFFAFLASFFAAG FVFFSPRKALSGSKFTFLPT

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28838	59206	A	29013	767	1428	FTPLSLRAVVIQLANRQYLDEK SDRAVHQGHIPRQFY*SLRRNL TNRHIQLIAIGGAIGTGLFMGSG KTISLAGPSIIFVYMIIGFMLFFV MRAMGELLLSNLEYKSFSDFAS DLLGPWAGYFTGWTYWFCWV VTGMADVVAITAYAQFWFDPDL SDWVASLAVIVLLLTLNLATVK NVGEMEFWFAMIKIVRPLSGSR TKKMSKSDDNRRNNVIGLLEDP KSVVKKIKRAVTDSDPEPPVRY DVQRPKRSALLERAPERFQEVF ILKGREDKRLPLIHALESQGG GYPVGKPPISRREKRPCRASGA YSPPVLLILMDPLGNLPIFMSV LKHTEPKRRRAIMVRELLIAL VMLVFLFAGEKILAFSLRAET VSISGGIILFLIAIKMIFPSASGNS SGLPAGEEPFIVPLAIPLVAGPTI LATLMLLSHQYPNQMGHLVIA LLLAWGGTFVILLQSSLFLRLL GEKRVNALERLMGLILVMMAP
28839	59207	A	29014	1	632	
28840	59208	A	29015	1	1215	
28841	59209	A	29016	38	457	LNRLCLKLVHASQSSRAMVFSSI RSFMFFSTLFILVRRQFSR*TIML SANSDSLTSLLPIWLLFISFSLT ALARTSSTVLKRSGESGHPCLV PVFRGNTFNFSPFSIMLAVGGV LHCEINCRICSTGRSANPPLDSCI
28842	59210	A	29017	899	991	
28843	59211	A	29018	1740	1868	
28844	59212	A	29019	1	1084	MSAEITAPWYRLQLDLFTKLVA TCMEQFRPKTIPPLAIPERLNAH CEELYELIASLNNILNLYMPAG QEAHRFAMGELPDEVLEICQR LAKLTEMLRGLAELFLNDLSEK TGSHDIVRLHRLILQMNRLGM FEAQSKLWRLASLAQSSGAPVT KWATREEREGQLHLWFHCVGI RVSDQLERLLWRSIPHIIVTSAT LRSLNSFSRLQEMSGLKEKAGD RFVALDSPFNHCEQGKIVIPRM RVEPSIDNEEQHIAEMAAFFRK QVESKKHLGMLVLFASGRAMQ RFLDYVTDRLMLLVQGDQPR YRLVELPANASPTVSAACWW AYSHLPKGLI*KVICSARCISTK SLFRPSTARW
28845	59213	A	29020	1	2022	

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28846	59214	A	29021	878	1267	LNSWLPSPVPTV*SSVFNAL*TG* ISPAFNPFADM*SASGLP*IKSPL STSTLFFTSLRASLIRLAVRTSPN FSVA VSL**SKSIMLLCRSVVSM IRRSTVAAFTLAAISVARVALN RFLIKSTGNACK
28847	59215	A	29022	294	2305	
28848	59216	A	29023	5	337	GAPQHQQMMSTYRINGRESPML TYPSTPNFFWLAWQARDFMSK KYG\RRFPIARFLWRSTPAPGVR KTIFIFISLVFVLMCANSWITI RTSAAAGCHCQVVCAGMNTW RVG
28849	59217	A	29024	1	1753	MPSTRYQKINAHHYRHIWVVG DIHGEYQLLQSRHLQLSFFPKID LLISVGDNIDRGPESLDVLRLN QPWFTSVKGNHEAMALEAFET GDGNMWLASGVYRIPLAVIWI GSLTSKAYKAEVQQRREAFNR AKMDYDHLVRQIQVGGLEGF IAKRTMLEKMKDEILGLPEEEK RALAALHDTARERQKQKFLEG FFIDVASIPGVGPARKAALRSFG IETAADVTRRGVKQVKGFGDH LTQAVIDWKASCERRFVFRPNE AITPADRQAVMAKMTAKRHRL ESALTVGATELQRFRLHAPART MPLMEPLQPTVSVDKVVVEKK GTKEVAEAYLKLYSPEGQEI AKNYRPRDAEVAKKYENAF KLKLFIDEFGGWTKAQKEHF ANGVIAVVAAGIGYWKLGTGEE SDTLRKIVLEECLTNQQNQNP SPCAEVKPNAGYVVLKDLGSL PYLLMPTYRINGTESPLLDTPST PNFFWLAWQARDFMSKKYGR RFPIARFLWRSTPAPGVRKTIFIF ISLVFVLMCANSWITIWRTSAA AGCHCQPTGIAQALLSTRQHGG AQCPPLPLSPLSSSF
28850	59218	A	29025	865	974	IMPRISGSQSGEHQQLVATAR WFARA*ILIPL
28851	59219	A	29026	1936	2490	
28852	59220	A	29027	1105	1518	
28853	59221	A	29028	1	975	
28854	59222	A	29029	1	1965	
28855	59223	A	29030	3338	3553	
28856	59224	A	29031	95	1289	
28857	59225	A	29032	1	732	
28858	59226	A	29033	1	672	



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28859	59227	A	29034	2	265	ARNEVAQPGVHETLDELTRL AEGLLAAEEAGIPLVNVHVG MFGIFFTDAESVTCYQDVMAC D/GGTL*AFLPYDAGRRLQHG RYQ
28860	59228	A	29035	852	933	PAPYALLLLPMHPHGLRRRDR QGRIHNLNDRRRHWHVRVCH LLRRERSRKDAPADGHPPL\RA VGGRNQNF*FGLRTTTCFTQTD FLTFFNLTSVTSNEASFTQFRTQG LVVFHQSGAGDVTDRSLTRDT TTFNGDVQVQFLNHVDQFQRL TNYHAGSFTTEVLFRQLVDYD FTVARFDENASCGTFAATSAVV LIFSHCLRLLCRVVVLVTRVNF QFTEHSTTQRAFWQHAFNRDF NHTLRTASNHLFKGRLFDTTDV AGVVIVHFVSTLVAGYSNFVSV QNDDVITGIYVRSVFRFVLTAQ ATSQFSSQTAQSFTGRVNNIPV AFYGFWFSCAKYYRHGARWCS NGRKIDQRHTHCFFCPCIRTDFA VEIGKEEFIT
28861	59229	A	29036	1	797	MIVFIENFKTSSPKYADILLPDL MTVEQEDIIPNDYAGNMGYLIF LQPVITSEKFERKPIYWILSEVAK RLGPDVYQKFTEGRTQEQLQ HLYAKMLAKDPALPSYDELKK MGIYKRKDPNGHFVAYKAFRD DPEANPLKTPSGKIEIYSSRLAEI ARTWELEKDEVISPLPVYASTF EGWNSPERRTFPLQLFGFHYKS RTHSTYGNIDLLKAACRQEVWI NPIDAQKRGIANGDMVRVFNH RGEVRLPAKVTPHPVGTWTAE
28862	59230	A	29037	1	1019	
28863	59231	B	29038	1	2727	
28864	59232	A	29039	1	2250	
28865	59233	A	29040	1	2850	

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28866	59234	A	29041	1	1339	MTGKCGKFGNFLESWRAQKTG ICGKVWNFLENLLNGFGQNAY SDTDNEVQAEVVSDDKDELVG NWSKGHSCYAKRLAAFCPLR DLWNFELERDDLGYLVEEISKQ QTIQEEADHKNLESQTEDAIE KKTPFSGEKFKLAAEICISNKDP NINSQDDGENVPRVAVHPNGC FAWKLPVLSRKFERKPIYWILS EVAKRLGPDVYQKFTEGRTQE QWLQHLYAKMLAKDPALPSY DELKKMGYIKRKDPNGHFVAY KAFRDDPEANPLKTPSGKIEIYS SRLAEIARTWELEKDEVISPLPV YASTFEGWNSPERRTFPLQLFG FHDKSRTHTSTYGNIDLLKAACR QEVWINPIDAQKRGIANGDMP YVFSSQMAKFTPTGLSSLIWK AHKCGEALETQKQ*C*QSGAT LPAGPRARAWPPYPRLFPTGLA CVDLHGNARKAT
28867	59235	A	29042	378	530	AFLPYDAGRRCLPGTVSV*SGL YVRGAQHGRYQ*HHRCTSDK IWRADKG
28868	59236	B	29043	1	1617	
28869	59237	A	29044	417	607	
28870	59238	A	29045	954	1163	
28871	59239	A	29046	444	3793	
28872	59240	A	29047	475	732	
28873	59241	A	29048	1	219	
28874	59242	A	29049	1	2438	
28875	59243	A	29050	2	175	
28876	59244	A	29051	1	411	
28877	59245	A	29052	172	378	LSSLRELGPVVAALLFAGRAGS ALT/VRNRPDARYRATLQYGD DGGGSAASGYFSPFLGWGYFIT TVDG
28878	59246	B	29053	1	1641	
28879	59247	A	29054	1	3036	
28880	59248	A	29055	1	1419	
28881	59249	A	29056	1	1500	

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28882	59250	A	29057	2	1760	KSQLHDPCCAPIQQEAVRAVV GQPPQQHLGFPVERGVQCQREC DFEKELEARIASLSDSVSNAREE RMALRQEQLQSLMQR APVWLAQAQNSLNQLSEQCGEE FTSSQRTHGHSEGNITKRGLIG ELRFENGDPNDQSYGRIKDG MAEIGTFHGGDLRGLTNKLDY LQQLGVNALWISAPFEQIHGW VGGGTGKDFPHYAYHGYTQ DWTNLDANMGNEADLRTLVD SAHQRGIRILFDVVMNIITGYAT LADMQEYQFGALYLSGDEVKK SLGERWSDWKPAAGQTWHSFN DYINFSDKTGWDKWWGKNWI RTDIGDYDNPFGDDLTMSLAFL PDIKTESTTASGLPVFYKNKMD THAKAIDGYTPRDYLTHWLNQ WVRDYGID/GFRVDTPKCLRCN PSITIGTNYSAS*PQWSSIPGAL* G*/PAWAG/GLPWAPSVLI.LDI LRQGFTMLEENLGNTIQDIGMG KDFMSKTPKATVTKAKIEKWN LIKLSFCTAKETTIRVNRQPT WEKIFAIYSSDKGLISRIYKELK QIYKEKNKQPHQQVGEQHEQT LLKRRHGCSSQQTHEKMLNHQ
28883	59251	A	29058	1	1119	
28884	59252	A	29059	3	2599	
28885	59253	A	29060	225	1245	RGSTGAHPRSAGKHYAKTSAG NAAGDP*YQMGPHHRGCGKP VPLPDHQSENLRWW*RRAWCG SGGYR\MAEGRHAAQGIIDWL LDVDKLGAEERRKVLQVTE NLQAERNRSRSKISQAKARGED IEPLRLEVNLGEELDAAKAEI DALQAEIRDIALTIPNLPADEV VGKDENDNVEVSRWGTTPREFD FEVRDHVTLGEMHSGLDFAAA VKLTGSRFVVMKGQIARMHIRA LSQFMLDLHTEQHGYSENYVP YLVNQDTLYGVGLYPLGALAS GWLPKRERKDATPGPTGYPG AHGNLELPERSEGPRAGGEPRR RTGHTQKGSPPDRGQTPPKGP
28886	59254	C	29061	201	1244	
28887	59255	A	29062	1	2530	
28888	59256	A	29063	675	920	RTYRLAGRQKQRRGGGTDSRS QNPWRSHRRHLP*RSSGAGKR GGKRFAGGAERNRPRLCRKPEP PAGGDGRRRLAAAGAD

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28889	59257	A	29064	498	707	
28890	59258	A	29065	510	554	
28891	59259	A	29066	600	734	PECLSAPDH*YKHCCSTGTQAR QPDADCPLLPRLAAHNERQTR
28892	59260	A	29067	1	1295	MCCNRCRNYAPGKGFSDVSFD LWPGEVLGIVGESGSGKTTLLK SISARLTPQQGEIHYENRSLYA MSEADRRLLRTEWGVVHQHP LDGLRRQVSAGGNIGERLMAT GARHYGDIRATAQKWLEEVEIP ANRIDDLPPTFSGGMQQLQIA RNLVTHPKLVFMDEPTGGLDV SVQARLLDLLRGLVVELNLAV VIVTSSPDQDWGFTPEPRLAAR FPGSTHSSRSRRNRGRRHPRPRS LPTPSAPHSRAPGDGVKLVP ARVTRNEPAPSDSVTLGVPHEP GACIGTPILTFVRPSTSAINAAA EESTGTILFGAGGFKRTDLNDT ESDSTTLVASRYWDLSSGWQR AINLRWSLDHFTQGEITNTTML FYPGVMISRTRSRGGLMPTWG DSQRYSIDYSNTAWGSDVDFSV FQAQNVWIRTLYDRHRFVTRG TLGWIETGDFDKVPPDL*LKSR VGQRSELGSQYTPRARVEPPKL LSRKVRAHFGSRAPGAGRA*RH LRAPDCGVRVWWAGSGAGDG GGRGCGGSGTSEWILGSGRRGE
28893	59261	A	29068	84	128	
28894	59262	A	29069	1547	1822	CSRCSIPAFRVKPAPLKPRVFSP AWNUPERLWHLAPSTFSGGEQ QRVNIAR/ELYRRLPHSAA*RN YRLP*RQNSAALSRLYAAFLPR PQYHH
28895	59263	A	29070	1520	1656	
28896	59264	A	29071	563	976	
28897	59265	A	29072	1	1011	
28898	59266	A	29073	1	1097	
28899	59267	A	29074	1	2490	
28900	59268	A	29075	1	879	
28901	59269	A	29076	1	1317	
28902	59270	A	29077	1428	1619	YAARRRALCGSPCFPGGCNGE NCRLPPQLHADLTARIFYETRG WWWSPRRWILNE*LPGWQ
28903	59271	A	29078	468	638	AQTSPDCGRCPWLSDYAKSG* HQLWARWQNNGLAHTPRADS THQQSALDGRISLT

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28904	59272	A	29079	1886	2329	PLLVWINTRPSLT TGRESASPAT LVCHATVPSLVIASHVLSFL*W SFTVLVISRIGVAFAHAIFWSIT ASLAIRMAPAGKRAQALS LIAT GTALAMVLGLPLGRIVGQYFG WRMTFFAIGIGALITLLCLIKLL PLLRRTVKYTSGC
28905	59273	A	29080	1	2319	
28906	59274	A	29081	3	194	STSSLAAQSLRFGYETSQTGLA TYCGEKIQ*FFADLQQPVCADS YPLLVMKKLGPVFFFDI
28907	59275	A	29082	3109	3384	
28908	59276	A	29083	703	1000	DCFLRRRIKRPFGTSMKDAQVR FEEGFMAMGALGLAMVGMTA LAPVLAHVLPV IIPVYEMLGA NPSMFAGTLLA\WIWAAVFLAK ELAGGVRLLVLI F
28909	59277	A	29084	2040	4603	
28910	59278	A	29085	3	94	
28911	59279	A	29086	3	148	YAEHMLEVMSSIGDYT/NPRPA SRPVTKFDQRGHLGHGVWNL MFERVK
28912	59280	A	29087	27	227	
28913	59281	A	29088	344	1067	
28914	59282	A	29089	798	1049	
28915	59283	A	29090	1	1473	
28916	59284	A	29091	1	720	
28917	59285	A	29092	45	208	
28918	59286	A	29093	1	2499	

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28919	59287	A	29094	1	725	MHPRFQTAFAQLADNLQSALE PILADKYFPALLTGEQVSSIKSA TGLDEDALAFALLPLAAACART PLSNFNVGAIARGASRRSAKNIP RAVRQVFWRILLFYVFAILIISLI IPYTDPSLLRNDVKDISVSPFTL VFQHAGLLSAAAVMNAVILTA VLSAGNSGMYASTRMLYTLAC DGKAPRIFAKLSRGGVPRNALY ATTVIAGLCFLTSMFGNQTVYL WLLNTSGMTGFIAWLGAISHY RFRRGYVLQGHINDLPYRSGF FPLGPIFAFILCLIITLGQNYEAF LKDTIDWGGVAGTYIASGGEP VNSHAFGVLRNVVSIIVFFHQF GDAIKRLFPTDLLPFIRTWRTVF RKLQTAFGVDEIHQASAFRTKC TAVDRVIRIAFDMDRLDFFSWR SGYISRIPLIGLYFACALERHQN ERQPIILLSDQNAIATINQLAIER DVLNCRVIIARSLSELVAIREEIF PLLIINNSHYLLDDAVNNYITVK NIITAAGIEQIKHFLATAFIRQQP ERFFSAPGSFHYSNVRGESWQH ITRQICAQLVAQHHITADEAQRI IAREGEGENLIVNRLAIPHCWSE QERRFR*TVAWWRAA*CAVCD DGDGRSVLPDLHVWQPDGIPV AAEHLRDDGFFYRLAGDCH
28920	59288	A	29095	3	453	
28921	59289	B	29096	1	3684	
28922	59290	A	29097	1	231	LLVFINQEEADFHTQRGGPVFQ QATFTL*QLALFAIEPGLMTDP DIQVRGTTLPYGRGAHGVYT SNWKLTFRRILY
28923	59291	A	29098	1	2862	

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28924	59292	A	29099	1	1567	MKLNKAGFNVPEYSLLKMP VGCLISALKKAEDRQEVILRLF NPAESATCDATVAFSREVISCS TMMDEHITTEENQGSNLSGPFL RVRAGESIKFFNVLLADTPGLDI DTMDKDV AHDSRSIQLAMLRD DEILTHPVFNRYHSETEMMRY MHSLERKDLALNQAMIPLGSCT MKLNAAAEMIPITWPEFAELHP FCPPEQAEGYQQMIAQLADWL VKLTGYDAVCMQPNSGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVTLTTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLDAEIARIEKMGPVPIKCTTEV G\NTLTLEQVKAENRAVLVTVG LSSGSGPLPFEHSDVEIAVDLFQ RARQAQGDISIPQSALIIGGGDV AMDVASTLKVLCQAVTCVAR EELDEFPASEKEFTSARELGVSII DGFTPVAVEGNKVTFKHGDLR TAPFLGVADKRNKSAGNHP
28925	59293	A	29100	107	892	LAICTGTYSGRQVLPRFVDRGA SLIAEERNAGARRRAGIRTTSA GGGLCAYAIVEF*CWRNCARFE LN/AGISVPI/SEFIGATMQQTVH AEQSAISHAWLSGEKALAAITV NYTPCGHCRQFMNELNSGLDL RIHLPGREAHALRDYLPDAFGP KDLEIKTLLMDEQDHGYALTG DALSQAAIAAANRSHMPYSKSP SGVALECKDGRIFSSEYAENAA FNPTPDIQRAVLAEKADAPLIQ WDATSATLKA LGCHSIDRVLL
28926	59294	A	29101	1	3100	
28927	59295	A	29102	1878	2699	GTARNLTVSLSYSSSGTPSNA PNARMEELGPHPGEASSLFHPE SPLLDELFLPEYKAGRTPNPDI\ GHYVRRADV DKGSRLLRGLDS NKDQSYFLYTLSHEQIAQSLFP VGELEKPQVRKIAEDLGLVTAK KKDSTGICFIGERKFREFLGRYL PAQPGKIITVDGDEIGE HQGLM YHTLGQRKGLGIGGTKEGTEEP WYVVDKDVENNILVVAQGHE HPRLMSVGLIAQQHLHWVDREP FTGTMRICTVKTRYRQTISLGPL RKPPHNRCLEI
28928	59296	A	29103	358	1160	

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28929	59297	A	29104	234	930	KRAFLCSFCANRRNAANSALAL PGNCPVAHAQKRHSAPGTLSPD ARNEKQPLYG\GAAPETPNPRL PPLDSGILGGYIAPDNLITLSV GHSLFDERFGLAPQMPKKLQK MTRFPNDSLDAALCHGDVLLQI CANTQDTVIHALRDIKHHTPDLL SVRWKREGFISDHAARSKGKET PINLLGFKDGTANPDSQNDKLM QKVWVWTADQQEPAWTIGGSY QAVRLNQFRSVMN
28930	59298	B	29105	1	837	
28931	59299	A	29106	1	1701	
28932	59300	A	29107	733	1323	
28933	59301	A	29108	1	736	MKPSVILYKALPDDLQRLQEH FTVHQVANLSPQTVEQNAAIFA EAEGLLGSNENVNAALLEKMP KL RATSTISVG YDNFDV DALTA RKILLMHTPTVL TETVADTLMA LVLSTARRVVEVAERVKAGEW TASIGPDWYGTDVHHKTLGIVG MGRIGMALA QRAHFGFNMPI/R L*RAPPP*RSRRTLQRPLLRFY SVTRVRFRLPDPAVN**DASSV WRR TIRGPSLGLSPGWNTRVSL CAFFG
28934	59302	B	29109	1	1359	
28935	59303	A	29110	874	1926	
28936	59304	A	29111	1	777	
28937	59305	A	29112	137	376	
28938	59306	A	29113	1197	1391	EIRATIVRSSTEGGRNSGLQSGN FC*RHGS*KITAGYIVPLPEESA TATGASWTHPWGRQDASW
28939	59307	A	29114	1846	2126	LMELIEKHVSFGGWQNMRYHY S SQLKCEMNVGVYLPKAA NE KLPVLYWLSGLTCNEQNFITKS GMQRYAAEHNIIVVAPDTSPRG SHVADADRYDLGQGAGFY LNA TQAPWNEHYKMYDYIRNELPD LVMHHFPATAKKSISGHSMGG LGALV LALRNPDEYVSVS AFSP IVSPSQVPWGQQAFAA YLAEN KDAWLDYDPVSLISQGQ/LRCG NHG*SGVE**FLRRQLRLQI*KD WPQ*EAHVH



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28940	59308	A	29115	184	985	LGKRLVTYHTDANGQPVNQIL VEAATDIAKELYLGAVVDRSSR RVVFMASTEGGVEIEKVAEETP HLIHKVALDPLTGMPYQGREL AFKLGLEGKLVQQFTKIFMGLA TIFLERDLALIEINPLVITKQGD ICLDGKLGADGNELFRSLILRE MRDQSQEDPREAQAAQWELN YVALDGNIGCMVNGAGLAMG TMDIVKLHGGEPAFLDVGGG ATKERVTEAFNPPGYIGPYQGV PPAGPGVTRMGKSVRRIVQVG CQVAAGSH
28941	59309	A	29116	1825	3186	
28942	59310	A	29117	366	1903	
28943	59311	A	29118	1	2139	
28944	59312	A	29119	345	431	AASGSADDNLHHQYN*GDIAF CLHALLP
28945	59313	B	29120	1	2616	
28946	59314	A	29121	1	1521	
28947	59315	A	29122	1	783	
28948	59316	A	29123	96	215	
28949	59317	A	29124	1	292	MWWGGLLYWLAALVTLLWA ASQIQALKKLTCAISQTLEEQPV LNSKSWLTSLQNDYSLPDSLTE RIWLTLSQRISRGELREF*TGRR KLVTEQCLV
28950	59318	A	29125	3	529	
28951	59319	A	29126	1	884	MVDSLIARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLTGTGQTPAFGRRVSGVIEI GDGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERESRSEGLDLLRMKVEEG DVILVKKLDRLGRDTADMIQLI KEFDAQGV SIRFIDGISTDGEM VLDKLARGYADLSKAESQWDE MMRTAGSLKLGTHASELIRSL LYLLNYIDDEDYRRRILTQLNR GEGRHAVARAICYGQRGEIRKR YREGQEDQLGALGLVTNAVVL WNTLYMEEALSWMRRNGEEII DEDIARLSPLMHGHINMLGHYT FTLPEDILKGELR*RHLPPPSSSA SPALPIGIVHVKHLLGDNRYPI WIMQPSAHHPARQPEHDNHFR

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28952	59320	A	29127	143	523	NQTLMIKGAAHGIFNPLCIKAT AG\AGAYHGARKRLCANAALA N*RNAGISVSCATTAPLSLALFT GAGQIAASNTGELDVLQQLGFS PIPRILPGRSSARNRSARPRIGS AGAAVMFSNNELMDA
28953	59321	B	29128	1	4107	
28954	59322	A	29129	1892	2720	PTAWSPPRPTSMTSISWVICCM ERSNLSQMPATKGR\QARGAG \EVDVDWLIAERPGKVRTLKQH PRKNKTGINIEYMKASIRAQVE HPFRIIKRQFGFVKARFKGLLK NDNQMGDVFHAGQPVSGGPN DTIGKFADVACAGPLLAELDA LGKALKEPARPMVAIVGGSKIV GALILLIAGFAILRLLFRALISTA SALAGLILLCLFGPALLAGYTE RITRLFHIRCAGSAYFIKNIQQN GITPEDISKRN GRVFLLVFILPFS LRRVGHAHH
28955	59323	A	29130	1332	1635	
28956	59324	C	29131	1	1677	

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28957	59325	A	29132	1	1114	MAEACNIGLEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFVTPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGTLRDSNFVLEGLLEQQTG LNPVEIMTDTCCGLEKQEEPPS LLRLNNRIKQLLPPVDLTELLE IDAQTGFTEFAHVSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFVTPVK TINSGSNRKYFGSGRGITWYNF VSDQYSGFHGIVVPGTLRDSNF VLEGLLEQQTGLNP/D*NHDRH LRLSGETGRATIIASSK*SDQTA TPTGRFNGTVEIDAQTGFTE FAHVSESGARAQDLHISLALRY* WLKPVIS/ALEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFVTPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGTLRDSNFVLEGLLEQQTG LNPVEIMTDTCCGLEKQEEPPS LLRLNNRIKQLLPPVDLTELLE IDAQTGFTEFAHVSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFVTPVK
28958	59326	A	29133	1	2908	
28959	59327	A	29134	735	932	
28960	59328	B	29135	1	1413	
28961	59329	A	29136	1	1469	
28962	59330	A	29137	177	361	
28963	59331	A	29138	1	849	
28964	59332	A	29139	1	564	
28965	59333	A	29140	1	1593	
28966	59334	A	29141	1164	1635	EGPNRQNGRDYRSVMPTNL\LL RRFHEATAQNAPDVVVWGS PMREFLHVDDMAAASIHVMEL AHEVWLENTQPMLSHINVTG VDCTIRELAQTIKVVGYKGRV VFDASKPDGTPRKLLDVTRLHQ LGWYHEISLEAGLASTYQWFLE NQDRFRG
28967	59335	A	29142	538	1116	
28968	59336	C	29143	1	2967	
28969	59337	C	29144	1	2214	

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28970	59338	A	29145	1	469	
28971	59339	A	29146	780	1052	
28972	59340	A	29147	617	2408	
28973	59341	A	29148	2	488	
28974	59342	A	29149	1	1083	
28975	59343	A	29150	527	3213	SWRSVQLLPATSIPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGQWQY RMRRYQNILKEHGCVTPIIMS MRRWLAKNRPQADVVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCGPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC GCCCKTKVVSGEYTVSSTMTLT DAEIAEGYAVVALIKPGAQIGR SPVNCDVASCHVISFNLRLVELAI MRRLLCRIAVLMSYRIEQRLMF LERLRHVGLIAHPAKKAIKKTR KPGMKVTFEQLKAAFNRVLISR GVDSETADACAEMFARTTESG VYSHGVNRFPRFIQQLENGDIIP DAQPKRITSLGAIEQWDAQRSI GNLTAKKMMDRAIELAADHGI GLLRLAGGGKRLYWHLLDQLH RRNDNJSLLDLGNNAEAVILRED MLPRENFRPGDVRGVLYSVRP EARGAQLFVTRSKPEMLIELFRI EVPEIGEEVIEIKAAARDPGSRA KIAVK'TNDKRIDPPTQHEDEED EGLYDDPFPLNECSVGPGRHR FAPPEAQFRRPETLKGAPTSRIP ETSVGVVSAGSDFEPHLMRELTC RLTALTWCYPGSAYAVHQPDE
28976	59344	A	29151	1	812	
28977	59345	A	29152	1	1830	

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28978	59346	A	29153	1	1308	MMPLIDLEDPRLLVRREIGMLL HVDYLDLVHEKVTCRGRNGGQ DREKTTMEKVRSSGTICPQAPE VVNHYFTTDDGYRIISARFGVP RTQVRTWVALYEKHGEKGLIP KPKGVSADPELRIKVVKAVIEQ HMSLNQAAAHFMLAGSGSVAR WLKVYEERGEAGLRALKIGTK RNIAISVDPEKAASALELSKDRR IEDLERQVRFLETRLMYLKELK ALAHPTKKVTLSLHREGKQINH KAVQRLMGTLSLKAAIKVKRY RSYRGEVGGTAPNVLQRDFKA TRPNEKWVTDVTEFAVNGRKL YLSVIDLFNNEVISYSLSERPV MNMVENMLDQAFKKNPHEH PVLHSDQGWQYRMRRYQNILK EHGIKQMSRKGNCLDNAVVE CFFGTLKSECFYLDEFNISELK DAVTEYIEYYNSRRISLKLKGL
28979	59347	A	29154	1	836	
28980	59348	A	29155	1	1566	
28981	59349	A	29156	297	936	RTSSSLMRSSSLLRICSGVSPRS IPRWFTSVSLPSSFIR\RIITFRYT PGHVAPASRRSCYKYRR*PMRL YTMIQSL/VGSRPSGLRAFSSD CSPLPRTCSLRRRVLMITTSRS *SLTYGVDPSPVRPVLAASEYF SRR\YAGFQNPNNLLVSG*YQG NYRHFGILRGYPG/TLKNSNFQL TRSARISLSSRSICTSTGGNTTL PPSSPPDC
28982	59350	A	29157	5	861	SWRSVQLLPATSIPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIIQ/RPVMNMVENMLDQ AFKKNPHEHPVLHSDQGWQY RMRRYQNILKEHGCQVTPIMS MRRWLAKNRPQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC GCCKTKVVSGEYTVSSTMTLT DAEIAEGY
28983	59351	A	29158	1818	1991	SPSHIRRTAPNGLRHYQR*IQQ* APSDQQRDFLVPHGADSAMAK HGGSHRAVLPPQGW
28984	59352	A	29159	3	601	
28985	59353	A	29160	415	549	

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28986	59354	A	29161	2	501	
28987	59355	A	29162	1	1347	
28988	59356	A	29163	3	2461	
28989	59357	A	29164	1419	1640	IFCASLSLGLYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVLPPQGC DPHMESLI
28990	59358	A	29165	1135	2067	
28991	59359	A	29166	1	1364	MAGNRRFMCTPKTHGLSISQH GTFPEHAGCKIRCAGRSRVRP AELLAPYTGDI AEGISKAMRG GAKFLHHGIKRQORYVAEATE EWRMAPGP LEV AWFAGVIYHL YYYRARRFFCAAQPLVSGFHEAE LSLDDAKWVLHPGPDAGFHVF DVDGRFVLAWMLFQGSYLAG ALGDQPVHHLGQLLALWRPL QITQLIEVMLVGRGGDQAVGQ ATLGIDTNGGLYAKGPLIAFLG LMHLRIALLFVLGRTGCAYDG GRPQLAEKLYSELRAQGIEVLL DDRKERPGVMFADMEIGIPHT IVLGDRNLDNDIEYKYRRNGE KQLIKTG DIVEYLN AALLIAVT VLTSMEASDLVDLGMTLSPAD YAERLAALTQKCGLDGVVCSA QEA VRFKQVFGQEFKL VTPGIR PQGSEAGDQRRIMTPEQALSAG VDYMVIGRPVTQSVDP AQT LK AINASLQRSA*CRDAGTLRLRA WLC*FLQRRYHRYKGPAPVQV ELCQICQRNEFCTQRVPGMCHV
28992	59360	A	29167	627	854	NAGDRNRNPNPSCTAARQYG*S RFYNCRR*RHGRKNLSAERNGL PEYRNCNPDHRPSVFLAAGRCF APTMCHDASE
28993	59361	A	29168	1	1593	
28994	59362	B	29169	1	3789	
28995	59363	A	29170	940	1326	
28996	59364	A	29171	1	1377	
28997	59365	A	29172	1	2547	
28998	59366	A	29173	561	845	AKIVQLRPRLRPSRSARRCPSA PRSRQRRRSGPLPEPAPRVS*Q IFPSQYWR YRQSTENQKQRLDP RGQIVNVPARRIIRQKRKCKV AGSA
28999	59367	A	29174	1	1284	
29000	59368	A	29175	624	866	
29001	59369	A	29176	1	1384	

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29002	59370	A	29177	2268	2684	RCRRCKRRLRRFRSLLSLAG SPENHARFYCRNSLPDEWIFRII HPRST*PPRSREIRRCHCG*RQC SSDGRKITSVHRGRNADGRELT HQA VRL LAYLSDRFARHHRHL RNAHRRGPDRI PKERHFPA TKL RHTPAV
29003	59371	A	29178	1	2142	
29004	59372	A	29179	1	2463	
29005	59373	A	29180	3	126	
29006	59374	A	29181	1	2013	
29007	59375	A	29182	891	1000	FDSFHWHSHPMLCCDRGQHKE NPQSRGPISCQ*IQQ
29008	59376	A	29183	1	846	
29009	59377	A	29184	90	411	
29010	59378	A	29185	1	1580	MSKPKYPFEKRLEV VNH YFTI DDGYRI SARFGVPRTQVRTWV ALYKHGEKGLIPKPGVSADP ELRIKVVKA VIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMY LKKL KALAHPTKK AAEIPRSTFY YHLKALSKPDKY ADVKKRISEIYHENRGYGYRR VTLSLHREGKQINHKA VQRLM GTL SLKAAIKVKRYRSYRGEVG QTAPNV LQRDFKATRPNEK WV TDVTEFAVNGRKLYLSPVIDLF NNEVISYSLSERPVMNMVENM LDQAFKKLPHEHPVLHSDQG WQYRMRRYQNILKEHGKQSM SRKGNCLDN AVVECLFGTLKS ECFYLD EFSNISELKDAVTEYIE YYNSRRISLKLKDL YASCLTVQ LFGVSTVMGLLIRILGSIFQKAL NISKIESFVA VTTIFLGQNEIPAI VKRFMIAESHEVLPHLYGMGH CGSRRWYAEWRPLHRVHEPSG
29011	59379	A	29186	1375	3174	
29012	59380	A	29187	604	1268	
29013	59381	A	29188	1	288	
29014	59382	A	29189	1	2412	
29015	59383	A	29190	82	405	
29016	59384	A	29191	1287	1472	
29017	59385	A	29192	1	3156	
29018	59386	A	29193	1	1824	
29019	59387	A	29194	1	1922	
29020	59388	A	29195	1369	1743	

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29021	59389	A	29196	21	432	GPGCNGVHRLCTE\QRDVRGTV RIVLKTFFNNCRD TVFVAFEVNN TVSLLVATTDMTSGDTAIVVTT TGFVSAANEVQILAFFQGDVSF FPVATTTDTLSVTFFNFNYQG VNDFDFDFKQFLHSSFD FCFGR VFSNFE
29022	59390	C	29197	1	1743	
29023	59391	A	29198	2005	2571	
29024	59392	A	29199	170	486	LQTQKDGIPAVVERLEYDPNLP RTSRWFRNDFSVPVLQLLGSP*
29025	59393	A	29200	1	1713	
29026	59394	A	29201	1	6729	
29027	59395	A	29202	1	753	
29028	59396	A	29203	1	1470	
29029	59397	A	29204	665	1773	ASSQVKSGWLSAKIPVISSYGP LLSVRLLSHAWPNSLCPQLHCF LPGAIWSASSLLKSGNRPLIRLA SIVLPVPGGPISKRLCPPAAV/HF QSSLSLFLTDNITEIML*RPDTW THVMYVLHHADKPNLYHGLPE NPEISETVKFWKGIWKPLAAVG FAATFAASIFHYVGVPNRAD E EENNLHEEKDEERKCSQDIQLV KERVIFLTGQVEDHMANLIVAQ MLFLEAENPEKDIYLYINSPGG VITAGMSIYDTMQFIKPDVSTIC MGQAASMGAFLLTAGAKGKR FCLPNSRVMIHQPLGGYQQQAT DIEIHAREILKVKGRMNELMAL HTGQSLEQIERDTERDRFLSAPE AVEYGLVDSILTHR N
29030	59398	A	29205	948	1620	



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29031	59399	A	29206	1782	3667	HRRRCRHGYPPVPA YRCRIWKC GQFHPTGIAGCGRTGHRRLPW* RRLSAEQTWRTFYGALCAERQ RPGGP*RG\SRSIMIEIREGRGCD GPWGP HAKLKL D HLGKEVLES RLP GILELSRTFAHVDPSRFRLS HLSLHDGRYSDQSYRYNDTRD MVPINGSIHRIGREPHYHYQRG QQYIGLCRNCNVIDTHICIYLV D QPIMDDIRLLLLYSEISSAIHWLL PVVQGEHYMLVDPDTNEREER GRSETRGFPRVPLGRTVSTVWY PLSNAATLAATRCRSRSPHAF AE PSSNNGFITATPLGRTHFLGMA FPPSACWRLLR AEPERVEAVLS ASGMNKAMRCGVSLICNFRLD YAPIEKQWDLHFADYFAEDLK LLAPLAKDGLVDVDEKGIQVT AKGRIRRLRRIRHLSMMPDAAL VASYQAYDFLRIRHKQRASAK QPNHCGTQHGSNGSLRTLWNSI DSGSVLTWCASLIFSSRKSLSPI QLVRSVDRGDVKKRYSMREFS LGETHSEAEFRELLEQNPSFVFF KPQSFAPVKGASAVPLVGRASV ASDRSIIPPGTTLAEVPLLDNN GKFNQYELRLMVALDVGGAI KGQHFDIYQGIGPEAGHRAGW YNHYGRVWVLKTAPGA
29032	59400	A	29207	1351	1806	VIVGITSNSVTVA AVSSWCRTW VPVSVLCLNCYPASMALVRGVI RGV*TCLSLCPNCAAIFIFAFGA VIFCITSVGFLFPPMVYKSGLRF FVFT*MRDTGVPQRLRAPRRSL SAKLGPACPFAYIVPHIWCRI GWGTCVCLAICVCVCVAD
29033	59401	A	29208	1308	1647	RSWEVSIVEFYVVRPTGHV*HA SGNLSHHRKRHPLADQAARKG ETVPPRGRRS\WRTQAHP*HLR QHRGQHPASLPTRTGTPQPGRR AIYRIPVRTAGQFQRIEVGDFQR VGHQ
29034	59402	A	29209	1	2184	
29035	59403	B	29210	81	1356	
29036	59404	A	29211	1	2349	

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29037	59405	A	29212	514	1136	ILRIMQRGMKQFAGLLRLSGIK MLPSA**LGELLHAAGSFFQRC CLLFSTGGKIGVARRNFTGTGI DGI*TFADMSDGVSQRALHM* NALRQVAHFTAPVNGQGIRQV TTGDFANVSNNFCQRSKQHTA NAVPRHQQNQYHHQRDNRLPL LGKSVIICVVSDDIAIQFFTAEG VLSKRFAHCLMPSLGGLSKIGP SMPLFRIISQFS
29038	59406	A	29213	1	2992	
29039	59407	A	29214	1	168	
29040	59408	A	29215	1	537	
29041	59409	A	29216	1	1881	
29042	59410	A	29217	1532	2160	KHWSDSIPGTEADWSASTTSGC AGFAAFACSSS*VICLLSGAVA AYAPQLRHQAIRKVIIRRTSAFP LMD*TWSFLSSTNGLASCASIS SAGSGAGSASGVTKVSVDTS GWPIFVTDRLLSSCSTRFTLPAN RLITVEPSLKRPISWPFSSATEPS FSPAGQVQRLMIPSRGGVMVP AQTVMPLPTIVAPTGPYSSHLL GSFTLSP
29043	59411	A	29218	1	1713	
29044	59412	A	29219	2159	2715	TIPAKPVPSMVASGTVRFGFLT PVLTAADSTPTKAHRQSRILLMI A*PSVVSAVFQLAA*VAASNQC QPTIAVITTGIRTSTRPIVA/CITG FVTGAVEIVLVANSVIDISVGSP FSIPQMF SARLGIATMAICPIMV SFSVAAINSASHNRQGFALQFFF NDAACGSGEFRILMQEEHPDSV VFC
29045	59413	A	29220	2	102	DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGHHWRSGE SGVPAACINLVCSALYAAGNM SVDLCHRDFAFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESGM IGGAGSLAFPLPALIWCAVRYT PQVTCLLTFVTGILPISEPPSNRI FACWGKPAWTACCNSLRARR
29046	59414	A	29221	1	1464	

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29047	59415	A	29222	3	29	MQTEQQR/AVTRLCIQCGLFLL QHGAESALVDELSSRLGRALG MDSVESSISSNAIVLTTIKD/GQC LTSTRKNHDRGINMHVVTEVQ HIVI/LAEHHLDPPEP*EQQRR
29048	59416	A	29223	5	307	
29049	59417	A	29224	5	948	
29050	59418	B	29225	1	696	
29051	59419	A	29226	1	1083	
29052	59420	A	29227	817	978	LAGCYTMLPGNGPAGMHACIS KLDK*AAVKKRRISEIIHENRGRY GYRRVPLSLH
29053	59421	A	29228	198	362	
29054	59422	A	29229	1	2907	
29055	59423	A	29230	1	2541	
29056	59424	A	29231	1	1566	
29057	59425	A	29232	3	601	
29058	59426	A	29233	1	1347	
29059	59427	A	29234	940	1326	
29060	59428	A	29235	1	2547	
29061	59429	A	29236	527	1383	SWRSVQLLPATSIPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIIQ/RPVMNMVENMLDQ AFKCLNPHEHPVLHSDQGQWQY RMRRYQNILKEHGCQVTPIMS MRRWLAKNRPQADVRIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCGPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC GCCCKTKVVSGEYTVSSTMTLT DAEIAEGY
29062	59430	A	29237	1	2496	
29063	59431	A	29238	3	2056	
29064	59432	A	29239	1135	2067	
29065	59433	A	29240	1	1566	

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29066	59434	A	29241	1	1605	MKVPRGDVMFQLNLRKDDGQ FEDQLLLLVLPPKHRGHLQLV ADDVWFKNRRACKRQQRQQQ KQQQPPGGQAKARPAKRKAG TSPRPSTDFRSRDGIPEKATRTS CPSDSSVFLQRPLSSTGRGSS LSWDSSQVLVILSTLTPSGTIVT AEPKYPFEKRLEVNNHYFTTDD GYRIISARFGVPRQTQRTWVAL YEKHGEKGLIPKPKGVSADEPL RIKVVKAVIEQHMSLNQAAAH FMLAGSGSVARWLKVYEERGE AGLRALKIGTKRNIASVDPEKA ASALELSKDRRIEDLERQVRFL ETRLMYLKKLKALAHPTKKVT LSLHREGKQINHKAQVRLMGT LSLKAAIKVKRYRSYRGEVGQT APNVLQRDFKATRPNEKWVTD VTEFAVNGRKLKYLSPVIDLFNN EVISYSLSERPVMNMVENMLD QAFKKLNPHEHPVLHSDQGWQ YRMRRYQNILKEHGIKQMSR KGNCLDNAVVECFGLKSECF YLDEFNSISELKDAVTEYIEYYN SRRISLKLKGLTPI
29067	59435	A	29242	3	1119	
29068	59436	A	29243	1	846	
29069	59437	A	29244	1	3383	MSEKLQKVASARAGHGSRRREIE SIIIEAGRVSDDGEIAKLGDNVE AWYRARLAGAFTLQECVMAA STFFIPSVNVIGADSLTDAMNM MADYGFTRTLSTVDNMLTKLG MAGDVQKALEERNIFSVIYDGT QPNPTTENVAAGLKLLKENNC DSVISLGGGSPHDCAKGIALVA ANGGDIRDYEGVDRSAKPQLP MIAINTTAGTASEMTRFCITDE ARHIKMAIVDKHVTPLLSVND SLMIGMPKSLTAATGMD
29070	59438	A	29245	104	1381	
29071	59439	A	29246	1	375	
29072	59440	B	29247	1	5082	
29073	59441	A	29248	119	343	RMPKRRRWGKLSTIRCSTTCKK RLT*IVLPVRTPGRLCSSLKSV ASHCLASCKAYSINKPWKRQPS KRHYVTMR

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29074	59442	A	29249	468	935	VPLAVPYGRLWRTIFSPLPSSFR STRVR*EVSGRSSPSISLALVR PIT/SLIVNAHPVELLQVVFPTL DKHIAAARIHAVFDNRHFATRL FTRRVFRTVNKAAQVTLFNPTE AVDLFFHFNAVTGKFHLRQGD KEGYVQAHTNNGDLRVRTSNP
29075	59443	A	29250	407	2145	
29076	59444	A	29251	1	177	
29077	59445	A	29252	1	1767	
29078	59446	A	29253	1	2499	
29079	59447	A	29254	2	607	
29080	59448	A	29255	2	314	
29081	59449	A	29256	2977	3913	
29082	59450	A	29257	1	2091	
29083	59451	A	29258	1	751	
29084	59452	A	29259	1	927	
29085	59453	A	29260	1	1113	
29086	59454	A	29261	1	875	
29087	59455	A	29262	1	450	
29088	59456	A	29263	1	522	
29089	59457	A	29264	1	912	

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29090	59458	A	29265	1	2416	MLAQSLQALEQDGFNLNRIAYPV VPPHVEYSLTPLGEQVSEKVAA LADWIELNLPEVLAVRDERTRY DIAVPRKRYGHA VSRNTFALRS QERYGHSVLETVGNSGSSKQFS MDILDPCARGPGQISLITVNHKL HVRCEIAYSVQTMVVKGGS FAAFFIAVVLWMIGYVPNVEQS TQALLGMQFIMIALPTLFFMVT LILYFRFYRLNGDTLRRIQIHLL DKYRKVPPEPVHADIPVGARLS FAERVMEGLSDGGQSLQSPSAL FSKQTLKNMSIYKIPLPLNILEA ARERITWTLNLTLPVCVSFSGG KDSGLMLHLTAELARQMGKKI CVLFIDWEAQFSTINYVQSLR ELYTDVIEEFYWDALPLTTQNS LSQYQPEWQCWEPDVEWVRQP PQDAITDPDFFCFYQPGMTFEQ FVREFAEWFSQKRPAAMMIGIR ADESYNRFVAIASLNKQRFADD KPWTTAAPGGHSWYIYPIYDW KVADIWTWYANHQSLCNPLYN LMYQAGVPLRHMRICEPFGPEQ RQGLWLYHVIEPDRWAAIGSP ADREDAEEYLEAIMEARVTV AGMGLVMEVQDYFDGEADRL AKAWLP/EYTPQIKSLKDERKE AYRQIVEMSTEPQDVDLVRPA NKFEMTRVREGEKEADLPVWK HLLCDESGNYPALLNHWETK VFEIETKREGFAFWYRNPQYTG
29091	59459	A	29266	786	1265	
29092	59460	B	29267	1	10161	
29093	59461	A	29268	1	882	
29094	59462	A	29269	1	2484	
29095	59463	A	29270	548	945	
29096	59464	A	29271	17	352	DLQDTGCFMLMNTGEKAV/KS ENGLLTTIAC/GPTGE/VNYALE GAVFMAGASI/QWLRDEMKLIN DAYDSE/YFATKVQNTNGVYV VPALPGWSLLWTRTCHRIFRH RISGAAGYK
29097	59465	A	29272	799	984	QGDIALVIATNQFCIKLAPIIELN TDFLCLINHMVVGQHIAFTGVD DDTGA*TFEGLCRLIR
29098	59466	A	29273	1	975	

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29099	59467	A	29274	65	562	DFRWHGDSRKVHRKNRLIKPL MILLTRLSNRTNWPLTAAVIWP GKV*SACRKSANAPKNIRRLCV SGWKSANWMSTQSSSSSSSTSS SIIIIINSSSSLQCQPCASKYLAH YFTVSSIAAYSTPVVSTQEPWA TRHHPHHQQTDORRRPATRKSPR QYHNETNRQ
29100	59468	A	29275	1409	1641	PENGRPVYAGGRDAAWRDVY AEFPRLSLPDGFRAAAVHRADA ALHHADL*HHE*APSALGLCL* RLAGGDWCRDYSL
29101	59469	A	29276	1	3252	
29102	59470	C	29277	1	2760	
29103	59471	A	29278	1	723	
29104	59472	A	29279	14	338	
29105	59473	B	29280	1	1201	
29106	59474	B	29281	1	1866	
29107	59475	A	29282	1067	2753	
29108	59476	B	29283	1	1144	
29109	59477	A	29284	3	724	LAQLYGDPPAWPTPTRGVSEIR LALRFKSNDSLLRHFKDTSTLY LEIVDYPGEWLLDLPMLAQDY LSWSRQMTGLLNGQRGEWSA KWRMMSEGLDPLAPADENRLA DIAAAWTDYLHHCKEQGLHFI QPGRFVLPGD MAGAPALQFFP WPDVDTWGESKLAQADKHTN AGMLR/ERFNYYCEKIVLVD/CL Q/PLNSGHSIYDMRWPDALIKFS YG/QRTVQRCFITPRAQSA*SGT TSGDLTRR
29110	59478	A	29285	1	1863	
29111	59479	B	29286	1	813	
29112	59480	A	29287	1	546	
29113	59481	B	29288	1	2691	
29114	59482	A	29289	1	1212	
29115	59483	A	29290	1	2328	
29116	59484	A	29291	1	531	
29117	59485	A	29292	188	358	
29118	59486	A	29293	2545	2713	LLVVQFFFQHL*VPSGTSP*L*H LSGILWHFLLQALLYPRVFLVL LCRSLGAVCLY
29119	59487	A	29294	1	2046	
29120	59488	A	29295	3	654	
29121	59489	A	29296	2	182	
29122	59490	A	29297	1	1215	
29123	59491	A	29298	141	266	

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29124	59492	A	29299	669	887	VYRSSVYRDSGCLSGGDLRSGN ASGHAKRQSDGDLRSRAATGG DHSAGDWCGRRVQTSAG*LWR KARPWPNR
29125	59493	A	29300	2353	2758	SQAYHQVLPVCEAAPDDNHT LAALR*HGVYEKHMDDQDCWA SFLPEERLFWRPAPRSDRVEC VDSLPLTAVGKVDKKQLRQWL ASRASARQRRSPLAEARKPQY VHQMDNARTALQKPEQARA HTEVHWT
29126	59494	A	29301	5	793	FLQRFVADLPCGAQVVKFSTFR TQCRQTEATLKVLFLHGTFNVV TSIGATTQVTNDARTDLRKQLV IDILFGIRRTLLHFLDRHNRHF CRCSRNTFLFQLLRMIRDFND FELV/NPLSLDSVLGMQPLREEI QQADRDDDKHHQGAGLLELET ANRFPQGDADPACADHADDGR RADVGFEAIEGVGDQQWHL WQHAVEDLFELVGTGGANAGP GSIASSESSLESTPVVWNSA STPARQRTGRGRRRPRTAWRRP
29127	59495	A	29302	1	2457	
29128	59496	A	29303	1	292	
29129	59497	A	29304	1	440	
29130	59498	A	29305	593	864	RTSAEPINPAPPVIRIFLISARLC* WTLSPILTN*L*STSITSTSAVA SASSSCARVQSPVSFFGNWWM LGSTTRVSPLCHWAISSADF
29131	59499	A	29306	2	696	VPAGRYTGRDLHLHI/ILPFRES LPARHRVRRYRPLEAC*TPCTD GYHRIFYRLKGESAKDGSVMT LRSFLDKDGHPIVDINDQAR HLVRLMPVLRRLRDARFMRRJR NGTVPNVPNVEVTARQLDFLA RELSSHQPQLSDGQIRQGLSAM VQLLEHYFSEQGAGQARYRLM RRRASNEQRSWRYLDIINRMID RPGGRSYRVILLGLFATLLQAK GTLRLDKDARPLLLIE
29132	59500	A	29307	3	1405	
29133	59501	A	29308	1204	1411	LRPALYQPARLSDAVRKTG*F AVVSGSEHAESDAG*SGELLEQ LSEVLR*PDEIFLWRCRAEREQL GL
29134	59502	A	29309	236	645	



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29135	59503	A	29310	1	776	MELAAALRSENQPDEKPLGETL KDLFSRPVLPMTDVLPLNLN IEEFMGEQLHVTGDTDIYREHH AAEMSNIDGNTKLDALDIDSSQ GIVDASGTAHLSDNWPVDITLN STLIVEPLKGDKVKLKMGGAL REQLEIGVNLSPVDMDLRAHT RLAEAGLSLNVEVNSKQLYC/L AHCMSMPKESGADEKNSDNR WCRVYWLGAALYHQNRERR GGSGR*ADLRRKPDVAGTGRA KRALCL*ES*YLRSGRTGTRIH
29136	59504	A	29311	955	1095	HRRHIPFLIHHRDQPFHQRLRK SFP*RPNAKCITRCQQTHS*FFIR
29137	59505	A	29312	1029	1490	RLPPAVDPTARLRRPASGRYP CIPAFVGTPAVSLLCWPTGADD SYCRKSLFRRWRGIRAAGKAAF RGWSGL\DRQANPAQVEIIEIRQ L/VRKSPQTAHSPARIWRRRLRSA SSRTYARRCCRFQCSKGPADGF PSVGSGKYQRSRRARRPASAG
29138	59506	A	29313	22	443	RRRHSCNSPTDEGASHTWTQTL SLSDKCRQGTVSGRLSLRKSDC TPISHASCSSSLHGH*VSVAVR LRMTDFSRVTGKDVQRFDAAGL GWTLERLLSAHAAFRVALKAG DMAILASRPPTVTPNSMRLGR LYRSGVYGR

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29139	59507	A	29314	2	2104	STLAQQWQAGDSIWSRPAIRVF ATYAKWDEKWDYDYGADN NANFGKAVPADFNNGSFGRGD SDEWTFGAQMEIWCSYLLALR QCQADIHSAGCICHGVVLVND QCLPPVKCWGRGAKSPFCAIT FRVRWTIRKSTKCCANRAYKR NITVGRIRRLRRIRQLPDATLC VLSGLQTEHNRRWPNSVCHFSP DSTFYNDLSGRMKNVRLMFNG IHRDNGFSKRPTDLNYTRKPLV LAFQTAWFITVRVEIVGFRGINR LSLMLEQNNVLIGENAWGKSS LLDALTLTLLSPESDLYHFERDD FWFPPGDINGREHHLHILTFRE SLPGRHRVRRYRPLEACWTPCT DGYHRIFYRLEGESAEDGSVMT LRSFLDKDGHPIECRGI*PIKAR HLVRLMPVRLRLRECPVLMRR IR\NGTVPNVPNVEVTARQLDF LARGGQARYRLMRRRASNEQR SWRYLDIINRMIERPETRYTREI GFTSTNIDLIYGLPKQTPESFAF TLKRVAELNPDRLSVFNYAHL TIFAAQRKIKDADLPSPQQKLDI LQETIAFLTQSGYQFIGMDHFA RPDDELA VAQREGVLHRNFQG YTTQGD TDLLGMGVSAISMIGD CYAQNQKELKQYYQVDEQG NALWRGIALTRDDCIRRDVIKS LICNFRLDYAPIKKQGD LHFAD YFAEDLKLLAPLAKDGLGDVD

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29140	59508	A	29315	1	2237	MLTGYRAVSRHKSQRYTADDA EEMIGKLTGMPIPLNSLRQWIL GLPGDATDYKLDDQYRLSEITY SQNGKNWKVVYGGYDTKTQP AMPANMELTDGGQRIKLKMD NWIRADGYHTLQTLFQFLDYG DTISIELRDDGDIRLLTPVEGVF HEDNLIVRAARLLMKTAADSG/ LSSDGKR/RSSSCARVQSPVSFF GNWWMLGQTTRVSPLCHWALS SAISHRRAFAQVINIRFKRQTKA GDFQFTGAFIGSRQAISHRRFHL IDNPERFVIVHFARGTDKPRLLG VLCHDKPRINSNAVTAHAKAR LKNINARVTIRQANQFPDVNPLI GTNQRHFISKSDIHIAEAVFEPSI IAADRLNPLVNELIIMPDIKRL DAFVRIAHEELLYLLGILMNPA NKDHVLPILITGPKESADYFRV LDEFVVHTLGENARRHYRIIDD AAEVARQMKKSMPLVKENRR DTGDAYSFNWSMRIAPDI.QMP FEPHENMANLKLYPDQPVEVL AADLRRAFSGIVAGNVKEVGIR AIEEFGPYKINGDKEIMRRMID LLQGFVAQHPSYNDLLI.MEL LPHLLVEGMLISAVSAESI.PWL HLSCVANISKRQLICAVPLPKPP KAGLLGKNIMGTGDFEILFVIIT GAGRYICGEETALINSLEGRRRA NPRSKPPFPATSGAWGKPTCVN NVETLCNPAILANGVEWYQNI
29141	59509	A	29316	1	2892	
29142	59510	A	29317	19	649	
29143	59511	A	29318	2471	3036	KVTWVTCILPMTLSPSAAFSSL FRMKILSLK**KRILR/SSGKPAA RQGDMTQYGGIVQGSAGVRI GAPTGVACSVCPGGVTSCHIV NPLLGAQVLPGETDIALPGPLPF ILSRITYSSYRTKTPAPVGSGLPG WKMPADIRLQLRDNTLILSDNG GRSLYFEHLFPGEDGYSPQRVT VACAPRRGKTG
29144	59512	A	29319	1	1476	
29145	59513	A	29320	688	1578	
29146	59514	A	29321	1	1653	
29147	59515	A	29322	1	218	MLIVFSLPSDTLVLSPL*PNFRT RPFRPSSVPR**PKKDLKIATSA MMEAAAYSSVIANVVLPVMDA KWLAR
29148	59516	A	29323	3	260	

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29149	59517	A	29324	1	1545	
29150	59518	A	29325	443	1041	LSSLKIVKLLRSTANSQVIDFQR WLGHDKRATLLLWKLEAAGSP LRPLSVQVTTTPQVEAETDNHAD NSYNAGLFIVNSLYTAEGVMD KHSLWQRYVPLVRHEALRLQV RLPASVELDDLLQAGGIGLLNA VERYDALQGTAFTTYAVQRIR GAMDELA AAVTGCRAACDAT RVKWHRQ*GNWSRNLAAPR KLR*RVN
29151	59519	A	29326	1	2349	
29152	59520	B	29327	1	747	
29153	59521	A	29328	275	729	
29154	59522	B	29329	1	2469	
29155	59523	A	29330	1	969	
29156	59524	A	29331	148	1180	
29157	59525	A	29332	56	170	VHA*GSLFFPELSMHQDLSQGH EVQLPPVNRSLKPNQK
29158	59526	A	29333	1	3246	
29159	59527	A	29334	482	765	
29160	59528	B	29335	1	1713	
29161	59529	A	29336	123	287	GDCSGCVEKQERCCNRNTT**A SAPGN/ARWNSYVG*KHHSCQ WGDYRRQCFRGE
29162	59530	A	29337	1	3189	
29163	59531	A	29338	1	1344	
29164	59532	B	29339	1	1233	
29165	59533	A	29340	1	1572	
29166	59534	A	29341	1	3591	
29167	59535	A	29342	1	843	MNYSHDNWSAILAHIGKPEELD TSARNAGALTRRREIRDAATLL RLGLAYGPGMSLREVTAWAQ LHDVATLSDVALLKRLRNAAD WFGILAAQTLAVRAAVTGCTS GKRLRLVDGTAISAP/GGGS AEWRLHMGYPHTF/TDFELTDSR DAERLDRFAQTAD EIRIADRGF GSRPECIRSLAFGEADYIVRVH WRGLRWLTAEGMRFDMMGFL RGLDCEVPDPKRRTNSLWRITK MVIWSLQVAIRGTVSLTAYKTQ LKNARHRLNEAPRRRILQMVQ PLS
29168	59536	A	29343	2	3203	
29169	59537	A	29344	227	634	IKTLPLSPDKLTRISKSIYRKQR AALFTHSFTTWVLAILEHRRFF AK*TRISKAHVISCVAGHTLA AAPQPHYFTRETYSPERVSTLM TSPICTNSGTLTTAPVDRVAGLP PVPAVSPFRPGSVSTISSSTKFG

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29170	59538	A	29345	1	1425	
29171	59539	A	29346	918	1022	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29172	59540	A	29347	1	1203	
29173	59541	A	29348	918	1021	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29174	59542	A	29349	656	1629	GIINVRKNRHTGSPGHRGKPGT REDEHGV/ELDRRLNFEWWK PEYGINLYQDYYKQDGFVEIPD QNNPSLGDMMVIMQIGQNPVW NHAGIYLGDNQILHHAFGSQT MNDVKLIKLSGSLGRRFGVFHR FAVDSYPEAIRALSSQVDGFKE YMQSEIGSRSKFAIFVDGVNVG HHEEEKFKCAKEIRIVPIPTGSK TGGLFQVVLGAAIMVAAFYTG GASLALMGTMSSSLFMMGGA MVLGGVMQMISPPQGWNRFEV QSSKNKPSYAFGGA VNTTGGGI PSPGPVWISRRWRNFLSRFLC RGYELKLTRLARVFFRLYNST
29175	59543	A	29350	1	8043	
29176	59544	A	29351	1	876	
29177	59545	A	29352	2020	2224	CVESRCCHATRCGSK*YSGP/PE DIDLKTEAAGAGVACDAAEAP DEAPPAKLHVLPPHPIEIVLKITI
29178	59546	A	29353	1	2346	
29179	59547	B	29354	50	340	
29180	59548	A	29355	284	520	
29181	59549	A	29356	2	304	
29182	59550	A	29357	79	177	
29183	59551	A	29358	236	373	
29184	59552	A	29359	1693	1961	RRLAIFHDQVGGKRRLCQLKAF MQSIAVALNHDRHHWH\GNRE NKVNCQLICVDIIINTAQPITSES /DQRQH/TLLRRQTRDRRHWS HEP
29185	59553	A	29360	2	388	YTVSFLLVITQLGFCSVYFMFM ADNLQQMVEKA/TRDLQHLPA QGDSADPHPGHSFLHADNPA LPDPVGVYPEPQGA VRLLDIGQ HHHPWEHGSDL*VYHGGDSIS QQPTLDGKLEDLLAVLWYSHL
29186	59554	A	29361	467	3014	
29187	59555	A	29362	1	1174	

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29188	59556	A	29363	1	986	MKVTFEQLKAAFNRVLISRGV DSETADACAEMFARTTESGVY SHGVNRFPRFIQQLENGDIIPDA QPKRITSLGAIEQWDAQRSIGN LTAKKMDRAIELAADHGIGL VALRNANHWMRGGSNGWQA AEKGYIGICWTNSIAVMPPWVP KECRIGTNPLIVAIRSTPITMVD MSMIKHTLPQRAAGTDRKIAM SREAQLLERHGYAFNELDIGK REPVTEEEKLFVAVCRGEREPV TEAERVWSKYMTRIKRPKRFH TLGGKPPQPGKKIVIRPLPGLPV IRDLVDMGQFYAQYEKIKP/V PVE*WTKSASSRAFTDARAARK
29189	59557	A	29364	99	375	THQPARRFPAYHYAHPAAAAA PGDPLGADLQLCARHYHRQRH CVPRHAGYPRSDGLHPQPRGR WRIRCSDCLRVPASDRGDAGDY FHL*LADR
29190	59558	A	29365	871	1206	
29191	59559	A	29366	1784	1966	RPLDVFSMSSFTSNSPLTDLVG YLTFSAILFLSWRLSLLSDAA*TP YPPWGSVHCRRFCSL
29192	59560	A	29367	1	1276	FHIKLVLTGATWTALPYCHSHV GLRASLKPTPPFWGRAPLGTRP SQKTECRLINFPETPIFGNSFK YDIEVSNKSPDEEVKLRRHHIA RCMKNFKTDIYFVSTFEPSTKS VDLLTVETFAGTVCEYADMPK EWTTRGLYDPTHLSASCHIKV EGLFSFEDRTVATLIRLFIIIPVK SMRGIGLTHALADVSGLAFDRI FMITEPDGADIAVKFTGIRLKV PCPPDHPAFSITNHQTEVTALV VFECDIAVRGSDRLRLSPGGG SNTDWVIFGLLIKENPGSLLAV GVNLLGKILLSVVAAVSESGQN FLSVLPVRSEGPCFVVIDVDVEL PGLRDIADDEVKTGVIAVTPAVIP ALWEAEVDVNIAAFRSQKAYIS GQVNKSGQQAITN/DATDYSRG HQLPCLQSECFHGIYHRIDVA

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29193	59561	A	29368	1	1815	STLEDPHYHYHIAEVSPVVIISIY GATGEKYGFITYRCSEHAALSL TKGAALRKRNPSFQLSYGGLR HFCWPRYTDYGYFELQINRLAL FSTNVTAETPYMHLAPPVGTQL PLPHLSHDNSSKNSGGCLPGAS VSCNYREPAVRLALASTLPLLR AQSPFFMHKDKDPLFWFLTVP KWFRKGEVILSSRPKKTEGSW FPKTFFGFGKSHVLVKEFYNRK HHIAKQQHAVERTRELFCPKG LG\YSKPQTQGDYAIAQHF/L*T NLPTGCWAKYAVISFMRTD/TV DDKH\WPEEHLAKN*LGLLADS G\IR\IKLPWGAPHEEERAKRLA EGFAYVEVLPMKMSLEGVARVL AGAKFVVSVDLTGLSHLTAALD RPNITVYGPTDPGLIGGAPENG DSDSALYRLRKEMEELVVG SDIFGKHQHGTTDSTTCPSTLE EFETQWFITGGINRILLATDGDF NVGIDDPKSIEMVKKQRESGV TLSTFGVGNNSYNEAMMVRIA DVGNGNYSYIDTLSEAQKVLNS EMRQMLITVAKDVKAQIEFNP AWVTEYRQIGYEKRQLRVEHF NNDNVDAGDIGAGKHITLLFEL TLNGQKASIDKLRYAPG
29194	59562	A	29369	3	1993	
29195	59563	A	29370	1	1782	
29196	59564	A	29371	1	3858	
29197	59565	A	29372	1	705	
29198	59566	A	29373	104	471	LWWAGA/SYLCWMGYQMLRG ALKKEAVSAPAPQVELPKSGRS FLEAIIYFGSVFSLFVGDNVGT ARWGIFALIIVETLAWFTVVAS LFALPQMRRGYQRLAKWIDGF AGALFAGFGIHLISR
29199	59567	A	29374	50	620	
29200	59568	A	29375	194	767	LWW/AGGLYLCWMGYQMLRG ALKKEAVSAPAPQVELAKSGRS FLKGLLTNLANPKAIIYFGSVFS LFVGDNVGTARWGIFALIIVE TLAWFTVVASLFALPQMRRGY QRLAKWIDGFAGALFAGFGIHL IISRLALIVPGLLQKNGGWRRM AII SAVIALVCHAIALEARILPDG DSGQNLSSLNVGSLVS
29201	59569	A	29376	1	1038	
29202	59570	A	29377	1	513	
29203	59571	A	29378	485	1166	

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29204	59572	B	29379	54	275	
29205	59573	A	29380	2	215	IFLLLLPPHHLLLLLLLLLLLLLLLLLLLLLLLLLLLLLQ/MIPLEFCRLYRKQG CICFWGSLGEILLMAEGEAGAS PSH
29206	59574	A	29381	100	393	FLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL LFSSSFLLLLSSSFFFFLASSFSFSSF SFSSSPSPSPSPSFFLLSSSFFGV ISLDVVT LAWQSARITGVSHRT
29207	59575	A	29382	264	911	ILGFLRDGNFWRKSSQSFPPVHH LLICLLRKSSETMQLTDEHLIHD HPKRPPITELVVPGLHEHLRSN VG DYRCEP PHLTKRNIFCILSEA TDITY*LT SIFPGFCFRLT*LLPL TEITGEAVVQIPIKFCPMCFFQS CAKIWTRGMQWHLEAWRCQK PQSPKGGVTALAEAPKSGLLE GQFMPMPQYLA VQKKVWF DVSVDESKLVNRVYG
29208	59576	A	29383	1	261	
29209	59577	A	29384	3	195	
29210	59578	A	29385	1	399	LERLSAPCISLLLSRSLSSLSLSS LLFFFFFFLLLLLLLLLLLLLLLLLLLL LL/SPPPLLLLLLLLLLLLLLLLLLLLL LLLLLLLLLLLLLLDPGDTIQGA PSRGYHPRDTIQGAPSRGHHPG DTIQGVPSRGYHPGGTIQGAP
29211	59579	A	29386	15	159	SPLHLSLV*VKQLLLLLLLLLLLLL LLLLLLLLLLLLLLLLLLLLLLLLLLLL LLLLLLSSSSFLPS
29212	59580	A	29387	17	429	SFFFFFFFFFFFFFFFFFFFFFFFF/C LLLLLLPLLLLLHRKHLICVTLG CLRWLGQLCVRLQGSCAWLQT LGWVHTYACVCTFFLDQQVAG RILLVEDPRSSLLQCCLLLDA\P LCCRFQKNMHFIRT*R*VHCSGI TSIQFNLEP
29213	59581	A	29388	3	282	RELLRGGNVYIGP*SILSFFLLLL LLLLLLLLLLLLLLLLLLLLLLLLLLLL LLLLVN*GVCCTLLSGPEISCRS DFAQGPTPLQGAPQTALGNLAS
29214	59582	A	29389	3	264	
29215	59583	A	29390	296	421	
29216	59584	A	29391	3	210	
29217	59585	A	29392	1	252	
29218	59586	A	29393	1	1731	
29219	59587	A	29394	1102	1362	NLGTAATLFFLFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFLFLFLF L/VPLLLLLLLLLLLLLSSSSCSP PPSSSSLEKLYLSI
29220	59588	A	29395	3	2368	



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29221	59589	A	29396	1	318	MEKKSPAYFCCRDMQVIHSDA ALQRLLTRFNDPEGWSNLAKN QYLSTSMKQKIWQRALSHRKN NPKADSDAYETSADMILSELIS HGEVDDQMLLNATALIRSDDW DFLESALISWDNLPVVLKELQ QNTPRNDIWAKFFLRQENSSRA QVDEALRVYYALDPDALAQLD VLAKRPYKTAAFRGEKTHRVP RRSVRQNIIDQADRLHGAQRLV INTNRTRVVDQLIEFLHHQHVN AHLAEIVRHHQPNRAGTSDRHL NAMVNSRLDVRNNEQTEYKTV RGLTRGLMMLNMLNKLDSTSP CRMLVCCVPRAPPNPGGLNPR AHSLSNRSP*NPLKLLSPTGPFEG MRPLGTHFWGGIGHGQGPEWG PQFGLGMNLLVKSLSLGHWATW VLARAKILRFELGASMMVAST
29222	59590	A	29397	2	4002	WQE*VHYIWGVMHGDGISMK SRIPVWEEFVPRFQATLELVC AMIFATAVGIPVGVLA AVKRGS IFDHTAVGLALTGYSMPIFWW GMMMLIMLVSVHWNLTVPVSGRV SDMVFLDDSNPVTGFMLIDTAI WGE/DHGTFMGAAPIRILPAYG LGTIPVAGFGRMTRSSMLEVLG EDYIRTARAKGLTRMRVIVHA LRNAMLPPVTVIGLQVGTLLA GAILTETIFSWPGLGRWLIDALQ RRDYPVVQGGVLLVAT
29223	59591	A	29398	187	1710	
29224	59592	A	29399	1	791	
29225	59593	A	29400	353	646	FYWNWVPFTNWQNPRLMGQK *HARWLHLRSLLPAM*ATLL*R ENNR*LLLLTLTSIFKTFIRRLS VSKP*VKAKKKTRLIIWSTSKFL SCMMLKFT
29226	59594	A	29401	406	1023	
29227	59595	A	29402	1	1129	
29228	59596	A	29403	1759	2100	FAGIGRSPGEALVLLLIEKMRES GDIHSHHGWLHLPDHKAGFSE EQQAIWQKAEPFGDEPWVVR DSPGYFALMVRAKFNVCVIVFR R*AQQRHRYTDVVVEIACRIKR VAALA
29229	59597	A	29404	86	426	
29230	59598	A	29405	657	3595	
29231	59599	A	29406	1973	2582	

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29232	59600	A	29407	1	1483	MFVLADFGHTRRTNRS LGHNIL PARIAPDAINKWLSGFFSREVQ LRWVGPMTRRVKRHNTVPLS FADGYPYLLANEASRLDLQQR CPASVKMEQFRPNLVVSGASA WEEDRWKVRIGDVVFDVVVKP CSRCIFTTVSPEKGQKHPAGEPL KTLQSFRTAQDNGGGEGERA ANTGATHRGRHRSPSAVRYRD RLNMYVLRRMDLLYRVKTLW AALRGNHYTWPAIDITLPGNRH FHLIGSIHMGSHDAPLPTRLL KKLKNADALIVEADVSTSDTPF ANLPACEALEERISEEQQLQNLQ HISQEMGISPSLFSTQPLWQIAM VLQATQAQKLGLRAEYGIDYQ LLQAAKQQHKPVIELEGAENQI AMLLQLPDKGLALLDDTLTHW HTNARLLQQMRAGGWSVKEG REKEYFQSPRGWGRSLMPSLGI IIRPP*RKPKNTENRRRCISASVTS EKEAPETINQYKAAVRRPFLFL ATALAQSEVRVCIAWTN
29233	59601	A	29408	2	1406	
29234	59602	A	29409	1	1818	
29235	59603	A	29410	441	583	GVIYRFPWRFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPGGLSS VSSR
29236	59604	A	29411	835	1143	RQLPVSLYVRAVAFENGCFGSC SVGG*GPPAARLGEEQVRGGSS SPCIIRAPRRLHSFLLLLLLLLLL LLLLLLLLLLLLFHLSSSSSFST SSSSSCSRFSM
29237	59605	A	29412	3	1487	
29238	59606	A	29413	149	534	
29239	59607	A	29414	1002	1145	GVIYRFPWRFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPGGLSS VSSR
29240	59608	A	29415	2	289	
29241	59609	A	29416	1	919	
29242	59610	A	29417	329	405	
29243	59611	A	29418	48	268	
29244	59612	A	29419	2	4625	
29245	59613	A	29420	1	867	
29246	59614	A	29421	1	684	
29247	59615	A	29422	409	543	
29248	59616	A	29423	1	1128	
29249	59617	A	29424	2	664	
29250	59618	A	29425	3	202	
29251	59619	A	29426	222	296	RSPRD*LPFKFSDPSLQSLKRGH S

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29252	59620	A	29427	1	1774	
29253	59621	A	29428	3	184	MSENMRCLVFCPCDTLLRMMV SSFIHVPPKDMMSIFSICLSAASI SSL*ASVCSYP SLNF
29254	59622	A	29429	667	834	
29255	59623	A	29430	1	738	
29256	59624	A	29431	39	230	QMAQHLP HL VFGSHSGSLWEL LSH*VYLLILSLPPPHTPQQAPV WDVPLPVSKCSHCSIPTYK
29257	59625	A	29432	985	1205	IPGSRGKNWVVTGTGQGCHRG PAESDGPAG\GARHWEQPPA*Y LVLFLCSQRRWPGRQQRGQSG RSWPSVRAAP
29258	59626	A	29433	339	592	PLQAWGPSLCS*AIGTPSRKPSP STAHVKHRRLCIPTRRGFSSDN WDPVSSPTCNDARQLHAQVDL EIPVRTCSVWFFVLVIVC
29259	59627	A	29434	633	894	FAENDGFQLHPCPFFQGS*LLCI GLAHAPLAQRSLLLSTF*CLLLS IHQTHSPSSFCPLLARSCDPLEE KRHSGFRNFQPFCSGFSS
29260	59628	A	29435	517	603	
29261	59629	C	29436	1	1188	
29262	59630	A	29437	1	1722	
29263	59631	A	29438	1064	1330	MCGIIEGSLVLFHWSISLFWYQ YHAVLVTVVL*YSLKSGSVMPP ALFFWLRIDSAMRALFWFHMN FKVVFNSVKKVIGSLMGMAL
29264	59632	A	29439	1	1308	
29265	59633	A	29440	162	377	YSHCSYTRKIQFLCCPSIKTHL GTNLTS*TFFT*VNIISIYLEASLF FSFLDLGRADKGSSLTGVRSIIT
29266	59634	A	29441	1	480	
29267	59635	A	29442	731	850	
29268	59636	A	29443	531	845	
29269	59637	A	29444	11	649	
29270	59638	A	29445	1	2433	
29271	59639	A	29446	1247	2420	
29272	59640	A	29447	29	94	
29273	59641	A	29448	1637	1830	
29274	59642	A	29449	3769	4263	RGGRSSTSGKGTAGCPQSPCF CRCSTLRRTAASPGISPPCKICS CSPLESIWMSNGLCRSCPPSEDS TCGC*GCCCCCCCCCCCCCCCCR RRCPSLGSDAGTELETQRPAG TGPPTVAPATFLQSRRLMVGA GTPTLGVRTPGFGLQLGFFYWL EDVERDTS
29275	59643	A	29450	492	585	
29276	59644	A	29451	2909	3174	
29277	59645	A	29452	1	1617	

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29278	59646	A	29453	1	599	
29279	59647	A	29454	1	504	MWNCCLTNKLLFQESLQKTATR LSAFSWEEAKVQLSWVVLNLA TSAMPLPKFYPNEIKVTYLRCTG DEVGATSVLAPKISPLGLSS/VK ALKEPPRARKKQKTIKHSNIT FDEIVNVAQHMWHRSLARELS GIIKEILGTPQSVGCNVDGCHPH DIIDDINGGAVECPAN
29280	59648	A	29455	1	1269	
29281	59649	A	29456	434	655	PFSSPASSSGR*KTTSFPAKLFN ACRISLLASAEVNPNIISAYLAT WISQIPSCSCRVPDFLIWSTNR YSIRF
29282	59650	A	29457	1	801	
29283	59651	A	29458	2	722	GRVGGGGQGANYLRVVPESGV YSTPSRLPPLPPKVRPPTRFKSV YLEVAPKGE\VG\TSALGPQRI GP\LGPVSKKKLG\DDISKA\TG\ DWKGP*GITVKLT\IQNRQAQD *GGCLSASALIHKALK\EPDRDR KKQKNIKHSGNITFDEIVNIAR QM\RHRS\ARETLWNHLKRS GTAQSVGCNVDGRHPHDII NSGAVECPAVSDIFIVTVGVKG GPPSVFTEISWEVLEMVTGGVG
29284	59652	A	29459	1	330	
29285	59653	A	29460	140	214	
29286	59654	C	29461	181	381	
29287	59655	A	29462	427	957	
29288	59656	A	29463	3	241	WLAERAPEGSPETKGS\PPPPP RSVLHLSA\SSPGLRPPEGL*TC RGSPSADSPRRGKHGGKTTHLV SWLSQQIPMAR
29289	59657	A	29464	122	473	
29290	59658	A	29465	1	771	
29291	59659	B	29466	1	1017	
29292	59660	B	29467	1	2568	
29293	59661	A	29468	1680	1899	NASRMSAGGRTAQNAD*LSE*I SQ*PQQRYECDNQQLDQL/V/ EQFIQTLEKAITQHRQQLNQWT QKVDIARRR
29294	59662	A	29469	1343	1714	
29295	59663	A	29470	321	2645	

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29296	59664	A	29471	611	1215	RWCVWSLFLQML/EMCPEFLPS GGFVVSLSGSKLQFTFTVNVTA HKGSDPKRVKLKTLAVSVTA LKAACLELFLPPGGFVVFAFGR SEAADLCAEGASSGLGQPREGL PRCSGGLKGSSSAARMGAEEK GAPRASQGCEGRHHA VTSRHS DMGEEEGESQRYLSCPQPSCPI NLLQEDASKVIVFAESGINPDSV LDLIMLH
29297	59665	A	29472	335	453	KYIWNVNLQHSVSMLL*FITS*L SGMDSLFPAAHCV
29298	59666	A	29473	1	1041	
29299	59667	A	29474	3	874	TEGQKNLIVEVTSNDVRFYP WTIDNKYYADINLCVVPNKFL VTAEIAESVQAFVVYFDSTQKS GLDSVSSWLPLAKAWLPEVMI LVCDRVSEDGINRQKAQEWCI KHGFELVELSPEELPEEDDDFPE STGVKRIVQALNANVWSNVVM KNDRNQGSLLNSLTGTNHSIG SADPCHPEQPHLPAADSTESLS DHRGGASNTTDAQVDSIVDPM LDLDIQELASLTGGGDVENFE RLFASKLKEMRDKAATLPHEQR KVHAEKVAKAFWMAIGGDRD EIEGLSSDEEH
29300	59668	A	29475	1	1773	
29301	59669	A	29476	1	1023	
29302	59670	A	29477	2	616	
29303	59671	A	29478	1	972	
29304	59672	A	29479	1	339	
29305	59673	A	29480	3	441	PLTCTSRAAAAMHKYEKLEKIG EGTYGTVFKAKNRETHEIVALK RVRLDDDDDEGVSSALREICLL KELKHKNIVRCAGGGCSLPVW PLGGGGG*HWTSVRRTCLAEPF FCPRLHDLHSDKKLTLVFEC DQVKGGVWRTVALGR
29306	59674	A	29481	1	843	
29307	59675	A	29482	1	873	

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29308	59676	A	29483	13	945	NRGPAGVPAAMQKYEKLE KIGEGTYGTVFKAKNRETHEIV ALKRVRLDDDDDEGV\SSALREI CLLKELKHKNIVRLHDLVHSDK KLTLVFEFCDQDLKKYFDSCNG DLDPEIVKSFLQLLKGLGFCH SRNVLHRDLEAPATWLINREW GSWKL\DFGPGVRAFVGFPV\ RCYSAEV/VSHLWYRSPDVLF GAKLYSTSIDMWSAGCIFAELA NAGRPLFPNDVDDQLKRIFRL LGTPTTEQRPSMTKLDPYKYP MYPATTSLVNVVPKLNATGRD LLQNLLKCNPVQRISAEALQH PYFSDFCPP
29309	59677	A	29484	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIADCGQLE
29310	59678	A	29485	3	1225	
29311	59679	A	29486	1	864	
29312	59680	A	29487	1	1413	MVNPVFFDITVDGEPLGRISFEL FADKVPKTTENFRALSTGQKGF GCKSSCFHRIIPGFMY/QGGDFT RHNGTGGKSIHGEKFDDENFIL KHTGPGTLSMAIAGPNTKGSQ FIYTAKSEWLDGKHVVFGKLSR GDSLKEPTSIAESSRHPYSRSEP SLEPESFRSPTFGKSFHFDPLSSG SRSSSLKSAQGTGFELGQLQSIR SEGTTSTSYKSLANQTRNGSL YDSSLTPSDSPDFESVQAGPEPD PPLGYTSPFLSARLAQQREAER HPRLVPTGPTHREPSPVRYDNL SRHIVASLQEREKLLRQSPPLPG REEEPGLGDSGIQSTPGSGHAPR TSSSSDDSKRSPLGKTPLGRPAV PRFGKPDGLRGRGVGSPEPGPT APYLGRSMSYSSQKAQPGVSET EEVALQPLTPKDEVQLKTTY KSNGQPKSLGSASPGPGQPPLSS PTRGGVKKVSGVGTTTIEISV
29313	59681	A	29488	1	3126	
29314	59682	B	29489	46	114	

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29315	59683	A	29490	1	704	AALLALGPRNPWTLWTPLTPN YPDRQPWTDKHPDLLTCGRCL QTFPLEAITAFMDHKKLGCQLF RGPSRGQGSEEREELKALSCI.RC GKQFTVAWKLLRHAQWDHGL SIYQTE\QRPRRPRSWAWPRWI. QPCRQWWGQQLRPRAPV/HISG SGLTRRSPTCPVCKKTLSSFSNL KVHMRSHGTGERPYACDQCPYA CAQSSKLNRRHKKTHRQVPPQSP LMADTSQEQASAAPPEPAVHA
29316	59684	A	29491	3	1605	
29317	59685	A	29492	1	453	
29318	59686	A	29493	2	128	
29319	59687	A	29494	1	543	
29320	59688	A	29495	39	1092	
29321	59689	A	29496	165	439	PPRQAKMQNLAAPGSHSQSPW/ TLRPKAL*LTSPQIFSA*RLKTD TARSPRKPPSFQGPVSLASITVV GIDGQASKPLKTPQLWCQLRQ YSFK
29322	59690	A	29497	1	281	VSDHAGTPALVLHP*RQVPLF* GRGKYPSTSPSPLAELATSAR NLTRPRNACSPGFLPSRVPSVR DPTGNRTVQLTWQPLPEPL.EI. WPKAL
29323	59691	A	29498	1	542	MRAPPKSGQLQHCRPSRGALRS GDLPWEINPLSSCSLLHEKDPP MTSGPQTNQPKEHLTNFKSGV RP/LQGRLPWSFTLSGKSRFSGE GASTPTPYIS/GAPIPYFRTPTSY LCAPIPYVRTPTSYLCALTPFPL FWRHIRTSKRLN/LQQPGIPPEPP PPG/CLLQVPEI*PPGQGMPPAAQ
29324	59692	A	29499	1	1044	
29325	59693	A	29500	596	833	LLLDLPAED*CCLIASEAP*TITD AEL*VTLTVEGKSVPLINTEAT HSTLPSFQGPVSLASITVVGIDG QASKPLKNE

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29326	59694	A	29501	1006	1118	RSKYPNLVSLCPSPLFPRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCPTPYFHDPTPFPLFW KELATCAGNLATGTRNAGSPG FLLSRVPSVWDPTENRTVQLT WQPLPEPLELWPKA/HLTDSFP DLLGLAA\ED*HCTIASEAP*TI\ TDAELWVTI\TVEGKPPFPLINT EATHSTLPFFQ\GPVSLASITVV GIDG\QA\SKPLKTPQLWCQH* TIRRFKHSFLVIP\TCQVPLLG\E DTLTKLSASLTIPGLQLYLIAAL LPNPKPPLRPPLVSPDLNPQV*D IGVEWGKGD
29327	59695	A	29502	6958	7935	
29328	59696	A	29503	1	486	
29329	59697	A	29504	1	492	
29330	59698	A	29505	2	502	RRAHACARRRRRKEMLGVNVL TSHSSQERMKLTFKKKAVNFA DAAAAQGPLLAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIGLFADKVPKT AENFHALSTGEKGFYKGSFCFH RIIPGFMCQGGDFTRHNGTGGK TSKKITIADCGQLE
29331	59699	A	29506	2	727	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKV\PKPAENFR/A L*SIEEKGFGL*GVPCFHR\IIPGF YVSRGGDFTPP*MAPGGQVHL MGKKFER*RTSSLKHTG\PGHL VPWANAWTQTQMGSQFFICTA \KTEWLDGK\HVVVLAKVKER HEILWEAMERFWVPGNGKTS KKIISIADCGQLLISFDLCFYLNH QDHSLLCSPRESTPLPHLLAGS
29332	59700	A	29507	1	380	LCCSPCRRRLGREEAGEEPTSP VTQYLQPRSPREECKMFACAKL ACTPSLIRAGSRVAYRPISASVL SRPEASRTG/EGAATVGVAGSG AGIGTVFGSLIIGYARNPSLKQQ LFSYAILGFALSEAMG
29333	59701	A	29508	76	385	EEPTSPVTQYLQPRSPREECKML ACAKLACTPSLIRAGSRVAYTP TSASVLSRPEASRTGEGSTAFN GAQNGALHLMQRELHTSAIRRD IDTWCKFIGCSAATE
29334	59702	A	29509	2	230	
29335	59703	A	29510	242	427	SAPDLTCNSKTWKNRGIICFHP ASLVSLY*QPQLASWTMCKQD ENTQEGKSWDSFSRDVIHI



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29336	59704	A	29511	1	1497	
29337	59705	A	29512	199	766	EEPTSSCHPNISSRAVP EECKMF ACAKLAMRPPSLIRAGSRV\AY RPIS\ASVVISTQRLSRTG\EGST GI*MGPQNGVS\QLIPKGSFQTS CNQAGGHLITGCQIYLGAGCLQ Q*GVGWFLVAGIGNSLLGKPY LGYGQKTLSPESQQLVPP*CYP GDFALALKLKAMGL\FC\LMVA FLILFADVTEITA
29338	59706	A	29513	427	840	
29339	59707	A	29514	1	477	
29340	59708	A	29515	45	344	PKGTVIDLEKRRQ*DGTL LC\RR CGS*GLPTFKKSTCGKCGYPAK RKRKYNWSAKAKRR\NTFGTG RMRHLKIVYRRFRHGFREGTTP KPKRAAVAASSSS
29341	59709	A	29516	1	668	
29342	59710	A	29517	649	992	
29343	59711	A	29518	1	2994	
29344	59712	A	29519	3	486	
29345	59713	A	29520	2	898	NSRVDDFVCPRSRRSKRDLIEFS CRIILFPLPSLPPRISFHPSTLAR VRIGGAVRRPHQSHSISSSSFGA EPSAPGGGGSPGSLPRPWGPKS CSSSLCGARS*FFWRDVKN\TGL VFG\TTLIMLLSLGSFSVSSVVV S\YLILGFSSVHHQLSGI*QSSVI PSCNRKFRKKGHFPQKPNWNV DITLSSKSFSINNMNAAMVHIN RALKLIIRLFLVEDLVDSLKLAV FMWLMTYVGAVFNGITLLILAE LLIFSVPIVYEKYKTQIDHYVGI ARDQTKSIVEKIQA KLPGIAKK KAE
29346	59714	A	29521	24	93	
29347	59715	A	29522	2146	2313	VSSIFFMSMKLGGFFTQVANIIS VAWNLVFCIRFLENTVGIVTI*R RCPIPF SWAF
29348	59716	A	29523	1	4368	MLFSYLEKYFYVADEL SHC VEP EPSQVPGGSSRD RQQGKPPPLP ALKAKTSSRSGPYATEIKKSTD DSIFKVLDFNRSSYSDDNK/LI PPTSPRNRVQRKNR\PKSQVAV DLVTDDTTLRENGSKTLSPSKIE LKPVRSDSPFQAEGDMLVSESC QDNNVNIKSKFMNLSQKGTPK EGPGILQPFESYGTPSQGSKNM DYSQDSKSPGKNGASPSNSNY SYSVLKESDAENQVPCNTNNIG NLGEEEPKFHAH

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29349	59717	A	29524	33	3339	TDQAKVDNQPEKLVRS AEDVS TVPTQPDNPFSDPKLKRMSKS VPAFLQDESDRETDTASESSY QLSRHKKSPSSLTNLSSSSGMTS LSSVSGSVMSVYSGDFGNLEVK GNIQFAIEYVESLKE LHVF GAP VEGLNSSGWKKTGVIPY*KGAY LLPNKGQMGKKKTLVVKKTLN PVYNEILRYKIEKQIL* TQKLN L SIWHRDTFKRNSFLGEVELDLE TWDWDNKQNKQLRWYPLKRK AKALQRFQLKAMGNS
29350	59718	A	29525	946	1183	
29351	59719	A	29526	2048	3359	
29352	59720	B	29527	1	300	
29353	59721	A	29528	1	1495	
29354	59722	A	29529	1	2769	
29355	59723	A	29530	450	3061	
29356	59724	A	29531	421	1464	
29357	59725	A	29532	238	930	RLSLVSSHCGTILSSEVVCAPPT AYIDFARQKLDPKIAVAAQNCY KVTNVAFTGEISPGMIKDCG/AT WVVLGHSERRHVFGESEDELIGQ KVAHALAEGLRE*FACIGAEKL DERIEAGIH*GRLFFEQT KVIAD NVKD\WSKVVL\AYEPLLAIGT CKTSTPQQAQEVHEKLARGWLK SNVSDAVAQSTRIHYGGSVTGA TCKELASQP\DVDGFLVGGASL KPEFV\DIINAKQ
29358	59726	A	29533	1	929	
29359	59727	A	29534	3	623	
29360	59728	A	29535	3	202	
29361	59729	A	29536	1	1046	
29362	59730	A	29537	1	1320	
29363	59731	A	29538	1	1052	
29364	59732	A	29539	922	1245	NRCLGNSFKCFLCILQVGRAHA FLLCSDFMPC EAVCSSIHSFIPV TKTQGAAPHTRAHSLTPDPKPS CCCCCPRPGEDPGHMCVWVP WQPSVIYAKYWTEHAQW
29365	59733	A	29540	3	130	RPEPEGRGC*GILGGGGGAGPS GHYALQEAQETSQSGRESQA
29366	59734	A	29541	1364	1916	
29367	59735	A	29543	1	451	ALPAPRRKVGLNLAPVTEPRDQ PWAMIIDVFSRYSGSVEGSTSDP *PKGE\KVLMDKELPRLSIQS GKDKDAVDKLA\KDPGRPMGD AQGGTFSEVHPCSVAAIT\SA\C HKYF\EKAGLKLMPWEMFTDF LGQSIGSQGFPMFCLGIYFP

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29368	59736	A	29544	175	355	FSQQLLGQAD**SFL\GCSRLL TAVSRPKRPGEAGITPRVRCLLS NMKDILVASKFWQL
29369	59737	A	29545	482	1196	
29370	59738	A	29546	196	818	
29371	59739	A	29547	170	370	
29372	59740	B	29548	147	257	
29373	59741	A	29549	1	1278	
29374	59742	A	29550	2	152	
29375	59743	A	29551	2	187	
29376	59744	A	29553	1	915	
29377	59745	A	29554	62	430	RQQDELALIAETLKCVDH*LSL DVLPRGCA*HRELCIHDLLKGN PLRRNILAG*TQERMQLQVESQ SIPEEILGLQPQLGPMGGLWNV RFLIPTVLWGFHCSQERAFPR KLQVKSFPVAQG
29378	59746	A	29555	149	381	
29379	59747	A	29556	1	656	
29380	59748	B	29557	146	1320	
29381	59749	A	29558	629	1417	WCASHWGS GHAARHA*ASHPL HGLLCSPSLPEEHHPLLHGAQS HRPPKG*GM*AHGTGLAGSSTC SPAQGL*IHQSAPCV*LKVCECT NRHSVSSCSDDEDVCICSLCLGQ* GP/ECI*CRIFLGPFNRLLIEGAPH L/CRSAMLNPLQEGAREQASAR SGWLLRLLTQEQLLCRACIQTR RDREGKTRHRKGTPEIGKGRAF WKKSLLKILILFNCLRYWNAYM EIWVPALTGIPPNVTVNYATSSS KDSRTDGRVDLLMAVTDGM
29382	59750	A	29559	318	608	ISQARRAAPWGPVQPEPSR*APP PASGHPVPSTTQRLRSAGARRG TGGQLHLQPRCGDPLGETSWA PESRRSAASLLKPARPRAHWE QTTPDALL
29383	59751	A	29560	88	564	SCLPVLRRALFLSPWVVDGTG RRGAACGGRWGGSGRTGAHG VGGRLRHGGLQVPSPALQEGS* GSVRNRAQPGGLALLGDPVHP LQPLARVLSPSLPG/DQQGWPA APSVGPTKPTPTRNSSWPPSAA HSPGSCSCLSLHTSLESCRCPSIN TSLHKHA
29384	59752	A	29561	3	339	RYKDSRPHQTQEPSWLHLVDP APRLQVELPASPALCARIPQLG G\HGTGRRGQGAALVGEARAG LPSPSPFFFSFLLSFLSFFLPSPFL FFSLFFPFCPVNCGEQCPIGKM

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29385	59753	A	29562	327	890	VMRIQVLLYYLRFADQGTGFH LVLCLRHTAGVQ*SWDS*SGLT PELV/HLDGSHV/LAASPRGSPG/ SPK*MGADQRSSSESSPGPQGG PRAEGPHHIQEAPRSA*AQGAG AEAARLGAGQASGCQSTRPA GSRREPGVSLDGGHRAVVGIQF QAPSRRAAWGHPLHDAPGRRL MSRQLLTPRRRRHRGD
29386	59754	A	29563	609	972	HPGQWLRKVYVWPQQCRPTG AVLDFSPGCCLPAGQGSGPAA RHA*ASHPLHGLLCGPSPDEH HPLLHGAQSQRPPKG*GMRAH SAGLAGSSTCSPGAGSTR*SQL GS*VW*GRGESLCL
29387	59755	A	29564	1	2715	
29388	59756	A	29565	3	644	KMPASPLPSAMNGSLLRPPQKQ KLLHFLYSLQKGISPNAIPPHSP HPTTAPVYSSQCERRRRQVISAF PT/GD*SLHSN*E*QGGVEGEAP AGTWAVRGA*GPAGVPGGRGL GGLRTRSSWPALLAPGRQSGSP AARH/GLSLPQPPWAPVQPEPP* GAPPPAPRRPVPSATQGLRSAS ARRRTGRQLHLQPPCGIHLVKP AGLLSLVGTWRVFMS
29389	59757	A	29566	1	470	MGQPLLLVRDSGGLQLWQKV KGEVQQHERRIIPAREEKVK RSPAGPPPSGGLDSSRHKIPSHE QA/SGVQPACRTNHQPRGIWCS PSLPDEKCPLLHSAQSHRSPKG* GVRAHGVGLAGSSTCSPSAGSN G*SQLGS*V*NKGR*IYPRTGRC
29390	59758	A	29567	777	1063	QLPPPSVFPTTPKTELVLGTPGH GQPHRGGHESDSAGGHLP/LR ALRSGWDPSPSSVCATPTSSGL SSTPQLPLHQRTSSSTASWSPG WGMGSC

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29391	59759	A	29568	195	1899	GSASGVVRSSRWARGLAGFRS EAADLHSECYSS*KQCGPKD*A EARFIAKSEGTKLPQCGRGPH*I QRFSTSPDSDGAQLASPSGSRTR AAGGAACQSWCRAP/STPQPLG GRWDWAPWSRGWRSSGTSGR TGAHGAGGR/PQAWRAAGPQP CPAGRQLRPETLKQNIILSLIQCI GASLVPTGTAELEPSPSLQLRGT TDAAQAIKNEFARVQKRNLCR RGPICFEGDALSWFFEKINKIDR RLARRIKKKREKNQIEAIKNDK GDITTDPTIEIQTITREYYKHLA NKLENLEEMDKFLDPYTLPRIS QEEVESLNRPTGSEIEAIINSLP TKKSPAPDGFTAIFYQRYKEKL IVLEVLARAIRQEKEIKGIQLGK EELKLSLFADDMIVYLENPIVSA QNLLKLISNFSKVSGYKINVQK SQAFLYSNNRQTESQIMSELPFT IASKRIKYLGIQLTRDVKDLFKE NYKPLLNEVKEDTNKWKNI PCSWIGRINIVKMAILPKIEKQTNW NSQTLQCQPFCESDVCTSTLQIQ ERFEVAPLHKKALSSEEITIDKT DPSAIEELTV
29392	59760	A	29569	77	640	
29393	59761	A	29570	384	746	APWSRGWCSSGRLGLHRSPWS GWEAQAWRAAGPEPRPAGRQL GAMSKVETGT*DSEQRHFRFG ESWGHPWAGAQTGPVLSGIL NVLSSFSVLALPRPTGWPRPCS AASPSRCPAQSHQH
29394	59762	A	29571	189	545	GLSCLPAGQGSGPAARHV*ASH PLHGLPCGSLPNEHHPLLHGA QSHRPPKG*GMQAHDAGLAGS STCSPGAGSTR*SQLGS*VCCTG RLVGTQQLRPESG*VSQPSRL WAAAEWSC
29395	59763	A	29572	87	374	AYSSQLGESRRYSLDQCLAK*I CEGRTCIFEEPCNCSSLYVRSNG GNHSHSTTTFKYNGSNWIPRW QGPGSTQPSKARRPVAFSQGN CAMEKGN
29396	59764	A	29573	1	2453	
29397	59765	B	29574	182	1356	
29398	59766	A	29575	28	340	IWISIGGFLFGCNFLFGAVLCFS LGLSCLPVEQGSGPAARHA*AS HPLHGLLCGRSLPDEHRPLLHG AQSHRPPKG*GMRAHGAGLAG SSTCSPGAGSTRNREN

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29399	59767	A	29576	142	442	PKG VGRALAAFPQDRAPGPAA RHA*ASHPLHELLCGQSLPDKR HPLLQGAQSHRPPKG*GVQAQ GTGTGRQLHLQPWCGIIHWVKP AGLLSSLGPRCFYKL
29400	59768	B	29577	1	2464	
29401	59769	A	29578	985	1292	WIPHRGCRWSCLPVLCRALTFL SPWVVDGTGCRGAGGGAHRG GSGRTGAHGVGGR/PQAWQAA GPEPCPMGRQVRPGEKSSAVPV GQPGWGTQYTLRSHWLGC
29402	59770	B	29579	1	2598	
29403	59771	A	29580	1	2028	
29404	59772	A	29581	5917	6355	QEAQPEESANDAQGDGPPGGK PQPQPEERSSCAQGVGPPGGQQ ESQDEERSSDAPEDGPPGGQQK PQPEERSSDAPEHDPGPGGQQQP QPEERSSDAPEHDPGPGGQQQP SEERSNDAPGDGPPGPGGQQQP*P EERSSGAPGHSSPDV
29405	59773	A	29586	875	2090	
29406	59774	A	29587	228	505	MLGRKPNHTSASRNTLRHCSR ARAQVKRMRQRREREAK\R QPGTASGTSGIAERDSGKCSRK RGVQKVPG**NTRQSKLRPREQ CTTADP
29407	59775	A	29588	188	592	AAPRSPSYRMIRKTR*MLGR/E AEPHVCQEHQVEALQHGQGP GETDATAAERR/RGRQRRQPGT ASGTSGIAERDSGKCSRKRGVQ KVPG**NTRQSKLRPREQCTTA DP*TLSTFPEGRGTELEPGFDSG ASVLMRGCRAALSASSSPQGP GPQEM*ATRNWGRQR*GRHC KLPVLITGLQGDVVEGVHVC ASQEPLIQNDQEDEVDAWQKA EPHVCQEHQVEALQHGQGP ETDATAAERRAGGKDASLVQH LVPVLLSVTQGSVPEKEEFKK SLVNEILGKVNYDQGNVPPQ TLEHCPPFPKGEARSWSLASTP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29408	59776	A	29589	524	1318	NGCDSSGEKSGRQRRQPGTASG TSGIAERDSGKWSRKKREFKKS LVNEILGKVNYDQGNVPPQT PSHHPNLEHCPPFPKGEAGAGA WLRLRGLGSYEGLPGCALCFFF PSRVLGLRRCEQQEIAGQQQGR DTQHGGQ/RSAEGRGRPG*GPG RTGPPAAQLPQSLRTTTRSRPW GRRQ*GRGR*PPQGLMRC*RRP HHTGWSPQNEKRQPGRSFQQH KSH*RE/RR/RARPVGQQVKAK RSQQFDDECGEDVRQEHSSRRD RVAVKS
29409	59777	A	29590	2	394	
29410	59778	A	29591	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAGELGFRFSGSG NRLDGKKESPSPIKPGDIKRGIP NHEFKLGKTPFIRNACPLVKKF EEDEAGGRFVAFSGEGQSLSKK
29411	59779	A	29592	1	561	
29412	59780	A	29593	725	922	VFKRVYIPFRSKLSSFFKCFP*W TALWEMLYAEEANPFSTIRILF QLEQPALGTSQYKILCLSST
29413	59781	A	29594	2	704	WRGSGSGGWESGRRGFFVAL PERSGVCQVVSIMFSNMFDP IPRVFQNRFTQYRCFSVSM LPNDIRIMPPSALDQLSRLNITY PMLFKLTNKNSDRMTHCGVLE FVADEGICYLPHWMMQNLLLE EGGLVQVESVNLQVATYSKFQ PQSPDFLDITNPKAVYLFQISGV LLDKGECAGECVCRLLENALRN FACLTGDDVIAINYNEKIYELRV METKPKDAVSHIECDMN
29414	59782	A	29595	1	1680	
29415	59783	A	29596	1	2220	

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29416	59784	A	29597	2	1114	SGRRGFFVALPERSGVCQVVSIMFSFNMFDPHPIPRVFQNRFTQYRCFSVSMALAWPNDRSDVEKGKIIIMPPSALDQLSRLNITYPMLFKLTNKNSDRMTHCGVLEFVADEGICYLPHWMMQNLL\EEGLVQVESVNLQVATYFQELSSCYLPHWLMQNLL\EEGGL\VQVESVQPFKWATY\SNFQPQSPDFLDITNPKAVLENALRNFACTTGDVIAINYNEKIYELR\VMETKPAKPVSII\ECMDNVDFDA\PLGYKEPERQVQ\HEESTEGEADHSGYAGELGFRAFSGSGNRLDGKKKGVEPSPSPIKPGDIKRGIPNYEFKLGKITFIRNSRPLVKKVEEDEAGGRFVAFSGEGQSLRKKGR
29417	59785	A	29598	15	569	
29418	59786	A	29599	30	525	YCLHHFFFQVSLLVFAWCSEMHGNRQLWE\RTGEMGRRTPLGSWTAKSPIGR/RSLSARVPRTVAHSQRAKGSHSLWVLRPQKRCAGKSPPPSRLARSRCPEPLVALARQPLCVRRAGPEERARAQRPPRPVPLLSQPGRALLLLLLRSFLRSPASGSEQQP
29419	59787	A	29600	1121	1420	
29420	59788	A	29601	758	1076	LPMNRPPRWTGTILAPIELLLELQQKENMALGSRTHHGSSPNSGSAFCQMACCSSLKPAL*SGRCSQP*WLWMSPLSRIFSISNSTSASSSIGNAIRRRSRPGP
29421	59789	A	29602	632	835	
29422	59790	A	29603	428	1214	FIAITVLPWHRSPQWYYPYWRGPVTA/LVRKVPAVAGERSLWSVVGLIWKPGLGLALQGVGFAVIGTFVSLYFASKGWAMAGFTLTAFGGAFVVMRVMFGWMPDRFGGVKVAIVSLLVETVGLLLWQAPGAWVALAGAALTGAGCSLIFPALGVEVVKRVPSQVRGTALGGYAAFQDIALGVSGPLAGMLATTFGYSSVFLAGAISAVLGIIVTILSFRRGQETAHQPDQQRAYDLQRSNRRVLPASPASACRCSDAHRSR
29423	59791	A	29604	1	825	



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29424	59792	A	29605	242	945	NGCIVRGKTSGSTFICVAMSVA ASTVRR*CWLPGRKAAAWRTC WAPMT*AVMC/WSRLMYGAR LSLLVGCLVVVLSLIMGVILGLI AGYFGGLVDNIIMRVVDIMLAL PSLLLALVLVAIFGPSIGNAALA LTFAGLPHYVRLTRAAVLNCL APLIVQASLGFSNAILDMAALG FLGMGAQPPTPEWGTMLSDEL QFAQSAWWVTFPGLAILLTV LAFNLMGDGLRDALDPKLLKQ
29425	59793	A	29606	1	2433	
29426	59794	A	29607	1	1383	
29427	59795	A	29608	1	218	
29428	59796	A	29609	1055	1873	
29429	59797	A	29610	3	823	
29430	59798	A	29611	183	1163	
29431	59799	A	29612	4375	5125	
29432	59800	A	29613	1800	2031	
29433	59801	A	29614	2	848	
29434	59802	A	29615	886	949	
29435	59803	A	29616	123	315	
29436	59804	A	29617	34	343	HLCSYGRVYAADPYHHALAPA PTYGVGAMNAFAPLTDKTRS HADDVGLVLSSLQASIYRGY NRFAPY*MTKP*KPSNVGRKEA FRGLSIAIHAVVHHFSNS
29437	59805	A	29618	1	305	AAAYRGAHLRGRGRTVYNTFR AAAPPPPIPAYGGVVYQDGFY ADIYGVMLHTATPSLPLPLPLP TVTVTDEFMTFSPLSPLTCSSPH LRRWCHECFCTFD
29438	59806	A	29619	1	2115	
29439	59807	A	29620	1	273	FFSRVVPPDSYQAQA/MVDIVT ALGWNVYVLTASEGNYGESGV EAFTQISREIGYPSLFGIQCGLHE CFAILCQVVYQFLLLMQLSDAQ TVY
29440	59808	A	29621	1	405	
29441	59809	A	29622	1	582	

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29442	59810	A	29623	1	3429	MAAGGGSGGAGRRPIAAAGGS ICYSHGRDLAPARPAQPPQPRD QPQVRPLCSPHAAAAAAAAAAL TWSCGPPAGFLTAPSAGSRVRL AARQQKAAPRKASAEPRDKKP LAPKLPQNALLVGKGESPRFIPL SVFFSKTFQRTARILKRSASDRL PWVTSRTCPGGIRTCPAEMTRY LRFANLTGGISEVSGFRDESGIN FGSWIAIPPVEKMVCEGKRSAS CPCFFLLTAKFYWILTMMQRTH SQEYAHSIRVDGD
29443	59811	A	29624	1	2740	
29444	59812	A	29625	1	1614	
29445	59813	A	29626	88	540	
29446	59814	A	29627	2	577	
29447	59815	A	29628	1	2169	
29448	59816	A	29629	1	1619	
29449	59817	A	29630	674	867	LDGDGIESINSLGQYGHFHDIDS SYP*AWNENVLPFVCILFYFVE QWFVALLEDVLHVPCKLDS
29450	59818	A	29631	746	1985	
29451	59819	A	29632	1	2211	
29452	59820	A	29633	139	247	KTSAAEKPKWRKE\RNARG* KRKRRKMLQRSQVNR
29453	59821	A	29634	335	556	
29454	59822	A	29635	1	586	
29455	59823	A	29636	908	1260	
29456	59824	A	29637	222	1686	ICRTCEVACAVSHHENQDCAA LSPDEFISPCWLARLVWRFCF FAQKAR*SPAKYGILGELTTGS KLVKANGLMEASTIAAILLGSV AGGVLAYWHVLVAWPHAHWP TVSRQQQLMASTLPFTSPLAQ IFPWRAITQRTMRMPFVIDARD ALLQGVFAAVNPSAHLNDSRH RRINKNVIEPGISCQRPQHLDRI AHPFGIHIHQLNAFTGRQFHRQ QLLYLRQTFVVDIDHHHPRLY AAVNGVIDSANAHRTCTRQQC NIAARFDAHAMLINILRGVIIGM ISTNNAAHRLCQRRRSKIRSRT GNTQPKLMQI

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29457	59825	A	29638	59	600	KWSRSEAGIDELCS/RNRVIIDH CWTTAVACHQCEDAPCANVCP VDAISREHGHI FVEQTRCIGCKS CMLACPFGAMEVVSSRKKARA IKCDLCWHRETGPACVEACPTK ALQCMDVEKVQRHRPRLNFLR LWYVVHAHTLMRMRPRFIQPW EEVVPRHHQHAACFQALIELLG RNGQILKP
29458	59826	A	29639	391	812	HSALCSCMRRRERLIRPTKTCK FNRLQRLCRPDKRSASGNFAVV IRLERVSLLAPFFYGVLLI.KCL MPKRQCNEADHHQHTTCAGQ KKMATHPLPGENKFIIGEDREY RWALMFPNENAPVCWVGHVR *KSPLHQHIDRA
29459	59827	A	29640	589	1075	
29460	59828	A	29641	1	435	
29461	59829	A	29642	9	661	
29462	59830	A	29644	403	567	
29463	59831	A	29645	404	706	
29464	59832	A	29646	114	851	CDHRNIVIRSAENISANFSHTGS V*GWMFTVP*SPSGRVVF*FCH L*ATCGN*LN*THSLSQGQRAI CILGFLPWHSRRIRSHVLENEC KVLLSGRSSQQMGE*GR*FSP* VGPLGGRALLQLPQPNSV/YVL PVSGLLVPAGE/CPLNV*PLVCS SANVLLSTSSCFCLCLARVSGF YRHRMGA/SGGFL/M*V*RKGS SFNFLHMA\ASSWDSYSGHIIFF *AGADYFFASSVSSLPLVLI.HSL HSFF
29465	59833	A	29647	1	1422	
29466	59834	A	29648	1	768	
29467	59835	A	29649	1	885	

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29468	59836	A	29650	1	1253	MVSVTALKAAFLFELFIPPSGLV VSLASGVKLQTFVSVTAHKG SVDPKSDQHGLVVSASGVKL QTFARRAEFPASQQQREVPRHD GGNHADRFTDHRQLMATGG RHFAIHVDRFGVPANGARRAG NIITQTVTNRFAGVESFQQCQLF GIYAVCERQGAIEPGPYARLFL ATFFIYTSSFKPPLPWLRLPRN TTPAVVRTAKGQVTAKYVIVA GNAYLGDKVEPELAKRSMPCG TQVITTERLSEDLARSLIPKNYC VEDCNLYLLDYRLTADNRLLY GGGVVYGARDPDDVERLVVPK LLKTFPQLKGVKIDYRWGTGNL QLTLSRMPQFGRQDTNIYYMQ GYSGHGVTGGSSRVGLMAGSQ ISRVSV/CINP*YHRFNLHWRYV ADAISADGAFRTVSGGGGRRSG
29469	59837	A	29651	3	354	IFSRTDISLYQHTAEQKHPYCW YPYPADSADI\SVNKHRRNATQ LHVSCSFLLSDQRFHHEAVPR RVVLFTFNTCVDKYIADIRSRT NGLGFLYAFKQRNSHFVFAAQ RHRHSACLR
29470	59838	A	29652	1164	1273	
29471	59839	A	29653	1	1161	MKNKLPPFIEIYRALIATPSISAT EEALDQSNADLITLLADWFKDL GFNVEVQPVPGTRNKFNMLAT RRHEGRYITCMQPLPIAEQEQE PEMTVRYIYISSADLTAEKFATA IRNHWHVENKLHWRLDVVMN EDDCKIRRGNAELFSGIRHIAI NILTNDKVFKAGLRQGWEDIED FGETHLDLFLKQYGDFENGIPVH DTIARVVSCISPAKFHECFINW MRDCHSSDDKDVIADGKTLRH SYDKST/RRRGAIHVNNAFSTM HSLVIGQIKTDEKSNEITAIPELL NMLDIKGIITTDAMGCQKDIA EKIQKQGGDYLFVVKGTQGRL NKAFEEKFPLKELNNPEHDSYA ISEKSHGREEIRLHIVCDVPDELI DFTFEWKGLM
29472	59840	A	29654	2	1587	
29473	59841	A	29655	236	666	
29474	59842	A	29656	1	1953	
29475	59843	A	29657	2202	2333	

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29476	59844	A	29658	1	1126	MHEVTLEDPSAQILITVITGHG EIITLKRSSRRQNDIRMYCRRRP EAFRDHHQLRFLPGTDQAIGIL MMSKVG TARPPDKTNIREMSV HTVVLICATRVFQCFNNAGNR DFIHRJAATRQAALHGREHRRRT PRGVTTIGKMVRKTKTAAGWE HESGFYLDG VVKLNRFKSNVA GKMSSGGAANGSYHSNGLGGH IETGMRFTDGNWNLT PYASLTG FTADNPEYHLSNGMKS KSVDT RSIYRELGATLSYNMRLGNGM EVEPW LKA AVRKEFVDDNRVK VNSDGNFVN YLSGRRGIYQAG KD LDRFKNLVLVHAARYAADL SYLPLMQELEKRYEGKLRIQTV VSRETAAGSLTG\GYRH*LKVG NWKARLACR
29477	59845	A	29659	1	1989	
29478	59846	A	29660	3	159	YKELNLADSSLSEEALIQAMVD IPKLMKRPKVVANGKARIGRPP EQVL\EIVG
29479	59847	A	29661	360	744	
29480	59848	A	29662	1	996	
29481	59849	A	29663	441	446	ICRQYPSDDRTASGAGGGDHQ QYGAGLRQTFCLCQRLSARTC* RLSASVCAT
29482	59850	B	29664	1	1608	
29483	59851	A	29665	1	2568	
29484	59852	A	29666	116	283	
29485	59853	A	29667	207	1270	
29486	59854	A	29668	114	503	
29487	59855	A	29669	1124	1216	LSGKMVM*SIKATCQRVPLKYF FTFECYML

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29488	59856	A	29670	1	1167	MPWLSTGAAALITALAVVELN DDDDHHHRNNSPLPPTPPDDES DDTPVPPTPGGDEIIPDDPDDTP TPPKPVSFNNDVILDKTEKTLTI RDSVFTYTENADGTISLQDSNG RKATINLWQIDEANNTVALE GNTSACRQALKIPKGSSDYTVT WKGGHFTFYRRWRCKVHKVV FEGSPPTICRYVLNRKNSWHV AHIFRRHAKPEEQ/CSHLFPYPF HHDLDEVLNDDPDVKLVVCT HADSHFEYAKRALEAGKNVLV EKPFTPTLAQAKELFALAKSKG LTVTPYQNRFFDSCFLTAKKAI ESGKLGEIVEVESHFDDYRPA ETKPGLPQDGAIFYGLGALFTNQ QGFFKSSLLSIFADSSSSVAGRS PHNLVKKRGGIVAISAFAG
29489	59857	A	29671	285	431	
29490	59858	A	29672	112	314	
29491	59859	A	29673	1	1191	
29492	59860	A	29674	282	660	GPSSEPSWAVAPGKAGDPHHIS AEWARNSTPSKDQA*RRPHTIC VTAYQGKVLLVGQSPNAELSA RAKQIAMGVDGANEVYNEIRQ GQPIGLGEASNDTWITKVRSQ LLTSDLVKSSNVKVTEN
29493	59861	A	29675	720	4525	
29494	59862	A	29676	218	990	
29495	59863	A	29677	54	723	
29496	59864	A	29678	1	2229	
29497	59865	A	29679	2	235	
29498	59866	A	29680	279	1275	
29499	59867	A	29681	692	1052	
29500	59868	A	29682	1	515	
29501	59869	A	29683	21	267	TLRFGANSVLKPEIKRGFEYSD CWVDDARLVLANAQMVRKG GEVLTRTRATSARRENG\GKKY SWQARGLESLSQPVERLSP
29502	59870	A	29684	1	1941	
29503	59871	B	29685	1	4107	
29504	59872	A	29686	840	1006	CHESHRQTDGGAVFRVYPGGG PRRECWFGSSLDEATPGWLLQ/ LYERDRH*PASTG

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29505	59873	A	29687	1475	2280	NAPGIKTSWRTLRLKRLLLLSRK TRMP/GFTNPRYGAGAATNPDP EVFSWAATQVVTAMEATHKLG GENYVLWGGREGYETLLNTDL RQEREQLGRFMQMVVEHKHKI GFQGTLLIEPKPQEPTKHQYDY DAATVYGFLKQFGLEKEIKLNI EANHATLAGHSFHHEIATAIAL GLFGSDANRGDAQLGWDTD QFPNSVEENALVMEILKAGGF TTGGLNFDKVRQRQSTDKYDL FYGHIGAMDTMALALNIAARM IEDWQLDKRIVQR
29506	59874	C	29688	1	2130	
29507	59875	A	29689	238	1879	
29508	59876	A	29690	22	219	RIFPTMCSMPTPIKQPRRW*VR KSVRTQVLSAADVRKLFLLK VQDPKIDRANPTMVNMRWMM SA
29509	59877	A	29691	596	723	MCASAP*WCELPAGVVRPPAST TADYFPLFTLVHGGCAHGRF
29510	59878	B	29692	1	441	
29511	59879	A	29693	1	1422	
29512	59880	A	29694	1	2856	
29513	59881	A	29695	2	367	QKAGAVQVLLSLWSSLSAAAA GTSLLKEPQWSQRIEALGDTGK ITEQGLSNTAIFSIRHTMAFLHS GSLDRPSALHSGTILSGKITS DICPHF*SPGRPCSKQHWAEMLV HHVCLPCRCT
29514	59882	A	29696	735	956	SRLLEITSPAIIFSPTLHSPA AHQYRKALHGRFPARSRDPPALA PGWRSARRER*SSPARAAARW CRKFAG
29515	59883	A	29697	217	378	ADGTGRRALGG*ATGPAGRWE SYSFTDSV
29516	59884	A	29698	279	732	PPGATLPTVARGTPQMGKEGSS PAKSLAPPLCEQMGQEDGHWG AGWGLAQVLLIALDGLLDAQQ HGGEPLGPAGRWSRIPSPTRCS CPHSAPRGPLAIFSSTCIPGNQR KLGTAPHTFGQPAWR*ACRCRS GRGPP*RSSLWRCTEEGAVH
29517	59885	A	29699	353	2776	
29518	59886	A	29700	158	605	PERSGLQEAGGSGRGWGKRS LPPAETAGLSGYMCFRAWLSLSR WDSGDHGWAGWGLAQVLLI ALGWSS*CASNGWLSHWFQPG R\*SRIPFTDSV*LVHILLPVG PLAIFFINLAFPGIRESWEQLL ILLEKPVGLEACPCKSGKGRP

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29519	59887	A	29701	1	753	MLALDQREAMRMIFPA\AGAP APALSPYAS/ARILVDQQFCYRQ VVEQNAIKSCAMIVA ADEFIP GNGIPVDSVVIDRKINPLQIKQD GGKALKLLVLWRSDEDAQQRL DMVKEFNELCHSHGLVSIIEPV VRPPRRGDKFDREQAII DAAKE LGDSGADLYKVEMPLYGKGPQ QELLCASQRLNDHINMPWVILS SGVDEKLFPRAVRVAMTAGAS GFLAGRAVWASVVGLPDNELM LRDVCAPKSGEPIL
29520	59888	A	29702	294	479	KIHFGFFCHCAESGSLDGRHFA PGV*RSEQHESGSGAVSGTGY WCSRDIYSREIDGLYRNW
29521	59889	A	29703	1446	2103	IHTDHRPGEIAATTLANRAALS GAALRRRRRRQNQTIAVGWRLA GTAHACNIISIRGYGSEDA/Q/ QRLDMVKEFNELCHSHGLVSII EPVVRPPRRGDKFDREQAII D AKELGDSGADLYKVEMPLYGK GPQQELLCASQRLNDHINMPW VILSSGVDEKLFPRAVRVAMTA GASGFLAGRAVWASVVGLPDN ELMLRDVCAPKLQQLGDIVDE MMAKRR
29522	59890	A	29704	370	1080	
29523	59891	A	29705	547	928	RLTKVEMPFYGKGPQQ\ELLCA SQGLNDHINMPWVILSSGVDEK LFPRAVRVAMTAGASGFLAGR AVWASVVGLPDNELMLRDVC APKLQQLGDIVDEMMAKRRFIP LLRRWVDLALTRWLITVSKP



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29524	59892	A	29706	1	550	MESGVATRPIADFDVYIDKLTE FVYKTNLFMKPIFSQARKAPKR VVLPEGEEARVLHATQELVTLG LAKPILIGRPNVIEMRIQKLGLQI KAGVDFEIVNNESDPRFKEYWT EYFQIMKRRGVTQEQAQRALIS NPTVIGAIMVQRGEADAMICGT VG DYHEHFSVVKNVFGYRDGV HTAGAMNALLPSGNTFIADTY VNDEPDAEELAEITLMAAETVR RFGIEPRVALLSHSNFGSSDCPS SSKMRQALELVRERAPELMIDG EMHGDAALVEAIRNDRMPDSS LKGSANILVMPNMEAARISYNL LRVSSSEGVTGVPVLMGVAKP VHVLTPIASVRRIVNMVALAVL FVNADETTVVNFHACFACVEV FTVRHTTNRVYQHGVVTLRFSG CFFAFHRHINAVFRFNIQAVFV ALRPEVIAIMHKLREQGHRVVV LSNTNRLHTTFWPEEYPEIRDA ADHIYLSQDLGMRKPEARIVQH VLQAEFGSPSDTVFFDDNADNI EGANQLGITSILVKDKTTIPDYF AKDKARHRTPLWAWLKLLW QRIDEDNMTTLAGNLAYVSLLS LVPLVAVVFALFAAFPMFSDVS IQLRHFIFANFLPATGDVIQRYIE QFVANSNKMTAVGAGQSGDQF LFALFNCQCFDADELKRIKNEL EPKMGMEMLNLVQLIAYTDWNE TQQKQPDGSWVNYNVDWMFK
29525	59893	A	29707	898	1163	
29526	59894	A	29708	81	454	NRLLAGRISSGTGDHFSGAAGI DSSLRPVW*T*TLRDQMSGGQS AKQPGRFAQWFYP*RLPETG*V PE*CL**CELIRAN/DHFLVSILPL RSPCVPLHLSTTPLRLAMDLTG LSGFPIPLSQA
29527	59895	A	29709	1321	2973	
29528	59896	A	29710	1	2218	
29529	59897	A	29711	68	432	
29530	59898	A	29712	740	859	
29531	59899	C	29713	1	3126	
29532	59900	A	29714	642	825	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29533	59901	A	29715	107	1315	KCADLPVRGLRHCWRRREDPS GADRSFSALIHSGRAAFWPCR* QGALMSIEDIFDAIIVGAGLAGS VAALVLAREGAQVLVIERGNS AGAKNVTGGRLYAHSLEHIIPG FADSAPVERLITHEKLAFMTEK SAMTMDYCNGDETSPSQRSYS VLRSKFDWLMEQAEEAGAQL ITGIRVDNLVQRDQKVVGV DGDVIEAKTVILADGVNSILAE KLGMARVKPTDVAVGKELI ELPKSVIEDRFQLQGNQGAACL FAGSPTDGLMGGGFLYTNT LSLGLVCGLHLLHDAKKSVPQ MLEDKQHPAVAPLIAGGKLV EYSAHVPEAGINMLPELVQIP CIERNAINAVKAVNAARMAMR RTSAPRVSLDKVIETMYETGKD MNDKYRETSRGGLAIKV
29534	59902	A	29716	3	264	
29535	59903	B	29717	85	737	
29536	59904	A	29718	171	820	LGVCAMTNSQCG/CDEYRSKN GYEGARKALTGLSPDEIVNQVK DAGLKGRGGAGFSTGLKWSLM PKDESMNIRYLLCNADEMEPGT YKDRLLMEQLPHLLVEGMLISA FALKAYRGYIFLRGEYIEAAVN LRRAlAEATEAGLLGKNIMGTG FDFELFVHTGAGRYICGEETALI NSLEGRANPRSKPPFPATSGA WGKPTCVNNVETLCNVPAIL
29537	59905	B	29719	1	486	
29538	59906	A	29720	1	605	
29539	59907	A	29721	285	449	TPAARDAQLSGGRGWY*CSAG NGLMQHRSQSGDWRAGRPFTE GW*PTPDWQIEA
29540	59908	A	29722	411	557	

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29541	59909	A	29723	1244	3261	KTINRTSLWYWTLHDHWSVTG RCAFTDVTKVEDHHEPQTQTR GLVMTT*ATT*KLTVSLTTAC VMNWV*MQVIPSP TAKIRL*LR TSNWLTSTTTLT/NNDVNGDSI DNGTEGSAVRVGLGTQFSFTK NFSAYTDANYLGGGDVDQDW SANDLTGITAKDAQMLS VVKP LQEFELFVLAALESRGTADILK AAGATTANITQAIEQMRGGESV NDQGAEDQRQALKKYTIDLTE RAEQGKLDPVIGRDEEIRRTIQV LQRRTKNNPVLIGEPGVGKTAI VEGLAQRIINGEVPEGLKGRRV LALDMGALVAGAKYRGEFEER LKGVLNDLAKQEGNVILFIDEL HTMVGAGKADGAIDAGNMLK PALARGEWHCVGATTLDDIAS TVKRCWTSHQHQTKNRTRRTT TRNIRFPNQMI EQINIALEQKGS GNFSAWVIEACRRRLTTGGPHV MYVLHHADKPNLYHGLPENPE ISETVKFWKGIWKPLAAVGFAA TFAASIFHYERVIFLTGQVEDH MANLIVAQMLFLEAENPEKDIY LYINSPGGVITAGMSIYDTMQFI KPDVSTICMGQAASMGAFLLT AGAKGKRFCPLNSRVMIHQPL GGYQQQATDIEIHAREILKVKG RMNELMALHTGQSLEQIERDTE RDRFLSAPEAVEYGLVDSILTH
29542	59910	A	29724	1487	1821	QYRPESVLEDPRRSDHHRRTDS FRETSFIVQSIVCRVSLSRAILQS KRL*EPGEFPPDPSSPEQRWPV CYPK*SDR*PEYPHSPGRQES QSRYLPAFRHRSYQTTAY
29543	59911	A	29725	4063	6544	
29544	59912	A	29726	174	556	
29545	59913	A	29727	1	1926	
29546	59914	A	29728	1	1443	

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29547	59915	A	29729	1	817	MAFNEPLMLEPAYARVFFCAL AGQLGITRLTDTVSGITLDAGQI AEPLALFGEDDDMDPRPSRSYQ VANGIAVLPVSGTLVSKTRALQ PYSGMTGYNGHARLQQAISDP GVDGILLDMPTPGGMVSGAFD CADIIARMRDIKPIWALANDMN CSAGQLIASSASRRLVTQTART GSIGVMMAHSNYGAALKTNGV EVTLIYSGDRK\VDGNPYEKLPI KDVRADFQTRIDATR\SAYTGM SVQDV/LDTEAAVFSGQESWDN GLAE*LVHTDWL
29548	59916	A	29730	68	98	
29549	59917	A	29731	215	871	
29550	59918	A	29732	1	2360	
29551	59919	A	29733	5	194	RGADAGERLNMLTVAEGVETP EQRDGAGRFCSLAKETVTPQW *GVLTSIIHSEACRIAANDE
29552	59920	A	29734	3	290	WRIIGIPLLLGYSLVCSRVLAC FWPGSDFWPRSRRKTSHLTVEA FPV/VVIFVSWRNPQVAP TSAH QNRPSRNPVSRPPNTQRVARRK HYALADGY
29553	59921	A	29735	403	588	
29554	59922	A	29736	1	743	
29555	59923	A	29737	5	97	
29556	59924	A	29738	756	935	
29557	59925	A	29739	1	1056	
29558	59926	A	29740	1193	1405	
29559	59927	A	29741	1	2718	
29560	59928	A	29742	3	357	

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29561	59929	A	29743	3	1307	KYGFVHYTLHTLGGTARALVA TDYRPLTKLSLDNGFQTV DHLQ ISQCPYIPPYNFPTDTSPTGPGLL QPPEGHAYDAYWRCVRAVRG QRVSALHGPVHLRSVYPSASA */WFAPRNPLGVWRSGYRIAPG YGS GVR SWVQPGGFARYKYDQ TGNASTVKCDYYRMAAFGHH AYRMQALTC SMTAC PCTTRQE TSSAWGSVSSMGDSRPPQEILG QPLLGRRIKYNCTGIGPWDGKG DESGASRPRKQQASGWLWACP RIFLVIPHSSH PAARRTNGSVGG SNRNRFVIITGPGPQLAPKGLW QWPIGQDPVTEIATLIGTHDLIM FDCIGSVSAPTIQPLEKLLSIVRY PAQVGLFFATRRCQAGATGKQ SQQRNPVLFIFYQRGISVFTSAF APVAVTAPPRQSRRQFPRLSPL DAHQRMGDVSIQAVKEARTC

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29562	59930	A	29744	1	2352	MLPDSSVRLNKYISESGICSRRE ADRYIEQGNVFLNGKRATIGDQ VKPGDVVKVNGQLIEPREAEDL VLIALNKPVGIVSTTEDGERDNI VDFVNHSKRVFPIGRDKDSQG LIFLTNHGDLVNKILRAGNDHE KEYLVTVDKPIITEEFIRGMSAG VPILGTVTKKCKVKKEAPFVFR ITLVQGLNRQIRRMCEHFGYEV KKLERTRIMNVSLSGIPLGEWR DLTDELIDLFKLIENSSSEVKP KRRPNRKQRASNVQSLRWKKR RKKAVARRPTQSSDDAIRGQQP DGVDCRDCRAGERQRQQTDSA MMELMVVHPHIFWLSLGGLLL AAEMLGGNGYLLWSGVAAVIT GLVVWLVLPLGWEWQGVMAFI LTLAAWLWWKWLSSRRVREQ KHSDSHLNQRGQQQLIGRRFVLE SPLVNGRGHMRVGDSSWPVSA SEDLGAGIRQCQQLVAHGLQLL NVSFDLRHLFQGRLEFGCALR LLTDSQSRLSRKPRGWRGLYG YSPPCGDIVRYHHHDL SVATLH VHINHDDCLEIAVLKGDMDGV QHFADDVIAQRGFFFAFSYEDT VIKIEKDFTMSGKPAARQGDM TQYGGSI VQGSAGVRIGAPTGV ACSVCPGGVTSGHPVNPLLGA KVLPGETDIALPGPLFILSRYS SYRTKTPAPVGS LGPGWKMPA DIRLQLRDNTLILSDNGGRSLYF
29563	59931	A	29745	1	3075	
29564	59932	A	29746	755	1321	
29565	59933	A	29747	397	576	
29566	59934	A	29748	1014	1266	
29567	59935	A	29749	416	724	TPGLTKTPCPWEKVTLFSLQWS AYRQANTSGLRHSASSLLPLAC RY*R*WRWQKLA AVL TASARQ SVKSLAYCWQRFVTWRWGRFS LRRVQLPFPLKWGLRR
29568	59936	A	29750	230	1829	
29569	59937	A	29751	1	474	
29570	59938	A	29752	137	586	KTKTNIKL*AAPITRMVMVRHA PHSGSVKK*SDITMSFATISVIG LGYIGLPTAAAFASRQKQVIGV DINQHAVDTINRGEIHIVEPDLA SVVKTA VEGGFLRASTTPVEAD AWLIAVPTPFKGDHEPDMTYV ESAARSIAPVLKKGAL
29571	59939	A	29753	2	557	

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29572	59940	A	29754	63	202	RGRSNSGSTSSVTSPVYT**PTA QGLSARQGCTKGHVRRYGF HD
29573	59941	A	29755	66	372	
29574	59942	A	29756	1	992	
29575	59943	A	29757	1	393	
29576	59944	A	29758	1	3753	
29577	59945	A	29759	1	1098	
29578	59946	A	29760	320	703	
29579	59947	A	29761	2	673	AAFLRECKDPQTMVPKAINSVI WRIGLFYVGSVLLVMLLPWS AYQAGQSPFVTFSSKLGVPYIG SIMNIVVLTAAALSSLSGLYCT GRILRSMAMGGSAPSFMAMKMS RQHVPYAGILATLVVYVVGVF LNYLVPSRVFEIVLNFASLGIIAS WAFIIVCQMRLRKAIKEGKAAD AHFTPYHATPLRNVMLHIYVLN GVSFRFVIDTNQIAQRCNRFAL LCGA
29580	59948	B	29762	51	623	
29581	59949	A	29763	1184	2406	
29582	59950	A	29764	103	473	
29583	59951	A	29765	444	699	CWPGKMSWGGFPLLLIGIVSE GIVPAPPCTSGRIQL*IRLVLDFF WLVGY*LLPQFQSLLLVYSGIQ LLPGLVLGGCMCRGIYA
29584	59952	A	29766	3073	3621	GVDNWRIPIISARLQR*AGSFFS FLGETGSLSCGLSLSFKSCCEAK NCSGSRGSSP/G*IPGVQEWNQI FSRF/HGVGLASLRKQRAPGDQ SPTGLLGE*AHGEIPVGNRSG KTRA/RGGPRGLEVSWSGSLTH SRG*ASLTSSHNSCHIRRGHPQ KRSGDMTHASAGH*AEVILAAP RRSCPL
29585	59953	A	29767	362	1850	
29586	59954	A	29768	1	1401	
29587	59955	A	29770	1366	1515	YDQAELDQLIHGSSSN/EQDPR/ RLPKGLTPQTLR/TLCQWIDAH QDYEFSTDG
29588	59956	A	29771	1	1827	
29589	59957	A	29772	419	1295	
29590	59958	A	29773	167	451	
29591	59959	A	29774	94	304	SPAASLYVTGSDLCTARMGGL VTRTGGLSRRAAYPLCHPPSGS RPSATSRASVDSG*TCGELGDA GTRAN
29592	59960	A	29775	345	652	
29593	59961	A	29776	596	2297	
29594	59962	A	29777	184	283	

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29595	59963	B	29778	16	1058	
29596	59964	A	29779	715	1234	FTWIGFYANRHFHCPVTTNDFP HFMKWRAAAHGGENIAFKLAN LPFFGDIRESHYQVVINRADRG FNPDDFTGARQQQKFVLIAGGF P*QLL*TNAVIGREFRNVQECIG LHTAGFANAVTKHF/W*M/PRL HCTIWRSGSRITGRSRWSTAI NCRVCSFCAISTLASRTSAR
29597	59965	A	29780	938	1250	PGRVSGKADGSV/LAGNGLLP FFCPLRLRGKYQPEV/IASIRRR YQLLFLAVASHQATAAGCGVN ALSDLRLCSVCRPKTHSVASG NGCRMALPSSPFSVIL
29598	59966	A	29781	1	1389	
29599	59967	A	29782	3059	3537	SEGKTANLFNKAITCSGAGECT RPWASDIKAQCAGGISRFATGN GFKRLCDTLRYLQAIENGLKN WRLIHIA TVRRCPFPPT/LSPATID AINVIGQWLAQDDFSGEVPYQ ADCVILAGNAVMP TIDAACKIA RDQQILAEGDFGLRCEIRDWCA NFVSDIR
29600	59968	A	29783	97	610	RCQTRQNAEYRVNAVLVHHFH AITHIRQQSQITRYIKLLRHH TQRRFTACRLRVDAPFPGNHQC CALHCLRKIDRIQHNFNARFNIR IEKYRRRNTH TARSAA/DPPSGR H*FQFAVVKHGRNFAAPVQVL RPSALPLFAGQTPPPRRVPLPA GYQRHMLLQYDQATVN
29601	59969	A	29784	269	753	YRTPTLQLDQGRADARRGVW/ HVPFSHESV/WENIVMTRQAQG ANFT*TLFCFGIGFAVIA*NCAI DPDISIRFFSKEETAT/GDRPDQI AAHLWRFP TPGGRFVHHRGAY AAIIFRP*YLNGRSMAEQSMILV TGELLVELNLEPSQVGNFAEK YYGPASQVV
29602	59970	A	29785	762	1182	
29603	59971	A	29786	3703	5889	
29604	59972	A	29787	925	1130	
29605	59973	A	29788	658	1212	
29606	59974	A	29789	904	1473	
29607	59975	A	29790	1205	2222	
29608	59976	A	29791	1	194	
29609	59977	B	29792	83	970	
29610	59978	A	29793	379	1095	
29611	59979	A	29794	172	367	
29612	59980	A	29795	557	1475	



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29613	59981	A	29796	1	738	MQPWALPTVGELWVCGRPGA ALRAGTEPSSRALGVSETALPA EIKLRVIRVGHSSPLAQLASFQK PVLFLVRLNSRRFLFLSLARSED GILFAKSKHSSPLSLTPLRCIVL MRMYEQLMSGDLCQRVMMPS RNNPGYWNPQ**SEIFKGSPAQ TMATLTCSFKKPPPKIPYKAIAL ATVFLIGAFLLIIRLPSCCQGYI KQRGGRPGPFQLLIHHSWCSY PGFYPPAHRFTMHPKGLPWVN PNE
29614	59982	A	29797	1	186	DCRLRAGDPRRSHCAVSPITGGS RALSGYRY*SVDQPRNDGVDQ *ATLRASAHLQTA VVEFSA
29615	59983	A	29798	724	1015	RSHPQCGYLQNHTSSASFSA RKG*NRHYAFARNDRLVPAPCS HHHQ*PAFPAPVHLH*PVDLST AIDAPAVNGDGKARPSKRRYQ RLSVPEVVQY
29616	59984	B	29799	1	4182	
29617	59985	B	29800	1	1191	
29618	59986	A	29801	167	504	
29619	59987	A	29802	1541	1852	FALFANRVSLAANVSGRGSPC WWRRIA VVCCSTNR/RSALDIA HQVDVLSLVHRLSQRGLTVIA VLHDINMAAR YCDYLAPCAA VK*LLRERLRKLCAAKPSK
29620	59988	A	29803	407	3584	
29621	59989	A	29804	3	150	
29622	59990	A	29805	1	921	
29623	59991	A	29806	300	560	IRDKNRVFLRESWRRLFTTAND QPHRPARRIISIAGIKWRYSDFLI NYCAGRAVF*RETGSVVERWH HHAGWKTPFRKRAGRTAGH
29624	59992	A	29807	100	315	PIKITSALASASRYVRATLSCSR NSTLRWKK*RKMALTKPSTIN GSRSNS**MNFFL*QAPPG*PSA LPFVH
29625	59993	A	29808	3	116	
29626	59994	A	29809	1	1469	
29627	59995	A	29810	1	2760	
29628	59996	A	29811	284	460	RNRQCYRARHLRWCLQYQKA CSGR*VPLRLPEVQSTDRLIS QRRRVSPDRQWWLACH
29629	59997	A	29812	438	1942	
29630	59998	A	29813	1	1464	
29631	59999	A	29814	3	602	

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29632	60000	A	29815	1252	1906	NTFKECKFSQAPFRFGNDPFLA SVVSRDGFVIAGGGGMVVVEE LEHALARGAHIYAEIVGYGATS DGADMVAPSGEGAVRCMKMA MHGVDTPIDYLNHGTSTPVG VKELAAIREVFGDKSPAISATK AMTGHSLGAAGVQEAISLLM LEHGFIAPSINIEELDEQAAGLNI VTETTDRELTVMNSNFGFGG TNATLVMRKLMIISASTTSILR
29633	60001	A	29816	1	2472	
29634	60002	A	29817	1	469	LFNREVCCLGQQQS*QMAL*LL GIESYIT*L*SGGDNASIGVIPDP AAIAR*RPWRSACG**PKCPLA DVFAGHSGRKRPPSMAFTATLI SPGTGRRAINSVLAQFKAGESNI WLSALPTPLTPTIRITNGALPSTF SGSSTFARISPISSFSRP
29635	60003	A	29818	884	1084	
29636	60004	A	29819	1	1040	
29637	60005	A	29820	2711	3854	
29638	60006	A	29821	1	957	MKIGTQNQAFFPENILEKFRYIK EMGFDGFEIDGKLLVNNIEEVK AAIKETGLPVTACGGYDGGWIG DFIEERRNLNGLKQIERILEALAE VGGKGIVVPAAWGMFTFRLPP MTSPRSLDGDRCMVSDSLRVL EQVAARTGTVVYLEPLNRYQD HMINTLADARRYIVENDLKHV QIIGDFYHMNIEEDNLAQALHD NRDLLGHVHIADNHRYPGSG TLDFHALFEQLRADNYQGYVV YEGRIRAEDPAQAYRDSLAWL RAGQVADKVVHASYYCTRNDLE LVAVCDSRLSQAQALAEKYGN ASVWDDPQAMLLAVKP*FVGL V\GAGQVADKVVHASYYCTRND LELVAVCDSRLSQAQALAEKY GNASVWDDPQAMLLAVKPDV
29639	60007	B	29822	96	821	
29640	60008	A	29823	3	775	
29641	60009	A	29824	961	2073	
29642	60010	A	29825	1	849	
29643	60011	A	29826	319	541	
29644	60012	A	29827	1142	1756	
29645	60013	A	29828	44	283	
29646	60014	B	29829	1	1812	
29647	60015	A	29830	685	1146	

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29648	60016	A	29831	202	918	AVDTGLADHRDRTEHGGFAAA IVHRIVKHFITAWAICQQRNHA ALVVIRRLEANHRRHRTGRG/S VDRVSAARSLSSGTMPGNGVW RIGVFTQLSVA/WHQ*VDLLIVF QFVRDTTDDHDVGIFALAAND RAAFDNILDPTGSVDVLLPLPG RHNIANALAAAALSMSVGATL DAIKAGLANLKAVPGRLFPIQL AENQLLLDDSFVNAAQQNILS VHILNQQTGKPAADVTVTLQE
29649	60017	A	29832	1184	2409	TLKACCLVRSMCRAVP*RC/GR QLVSSDNISNDPMNVIDWINMY ALAVSEENAAGGRVVTAPTNG ACGIIPAVLAYYDKFRPVNER SIARYFLAAGAIGALYKMNASI SGAEVGCQGEIGVACSMMAAG LTELLGGSPAQNMEGKIDRPEE YADIATKCVTNFREKNRDRCL VILSRNDEALNSQRTSEELHHY YEIVWDEEQTHKFKNISPHLQRI KAFKTLGGPHGNITVDMVISAQ ELLQEDMATFDGHIVEALMKM PEVNAMYPELKLHAIGWVKHK CIPGAKWPEIQAEMRIWKKRRE GERKETGKYTSVVDLARARAN QQYTENSTGKISPVIAAIHREYK QTWKTLDDELAYGRCFADRQN LMVCLRSMPNVFTGSCARMRC CLSENLLYRHRNGHIQAEWP
29650	60018	A	29833	1	3195	
29651	60019	A	29834	1	621	LLAGTALVGGVQPADAITVDA MIPNFNWAF LGVTTWIFMAAG GAESVA\CTLTTSKAVRNRSFK* SSSPGILSGYVSRSSGSPISLISP ASLCAGHMRFFCSSSKPTCSNP RTFAAALSSAWSSPSPNEGFSN PAFLGTSLMMFHLELRRCIPIV TTDLLPLTSGDVGLVLLCVGLD GSLWSDCRMTESVSTTNPPIIT SRNS
29652	60020	B	29835	46	893	

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29653	60021	A	29836	3	2037	CTSSPDPPSGLPPGFAKLTSLIVT LVEVGVSPEPDEGWLYLAVVID LWSRAVIGWSMSPRMTAQLAC DALQMALWRRKKPRNVIVHTD RGGQFGDRWKGWLTRSIFRWI SFQPALAPTRKAALCYLAREVN PDMADYIKKLKLPGIHVREESR RYYPSGEVTAHLIGFTNVDSQG IEGVEKSFDKWL TGQPGERIVR KDRYGRVIEDISSTDSQAAHNL ALSIDERLQALVYRELNNAVAF NKAESGSAVLVDVNTGEVLAM ANSPSYNPNNLSGTPKEAMRN RTITDVFEPGSTVKPMVVM TAL QRGVVRENSVLNTIPYRINGHEI KDVARITTEEDFNHASAARFVC AAAERRCKTTINLV PENEVLNV LEGEDAETNALRAKRRC PKCG TAMDSYLIDPKRKLHVCGNNP TCDGYEIEEGEFRIKGYDGPIVE CEKCGSEMHLKMGRFGKYMA CTNEECKNTRKILRNGEVAPPK EDPVLPPELPCEKSDAYFVLRD GAAVAARFNDDRHRRLAVLY ADQADLYGVADSVSAGDSL SA LYKHERRLVVPLL VSSSLFLY RHGIRLPCGPSGGIWAPWQIRR GRQAVNCLAPM/HHPGKNRAW KTYCSQ*AIVPQLPVCGI*PRSD SYHDYQRDPRCQPLRALWRRS DSPIGGYSSAIGI*TERHCRSGNP
29654	60022	A	29837	993	1832	
29655	60023	A	29838	124	276	QEGRCQVTITRK MPLSSDLGSL HGLAGNHSPPICARTPHVATVL RQLLELEDKHWNGSG*FARLG WK PQSPHLCQNPPCGHCPQTAP GA
29656	60024	C	29839	64	267	
29657	60025	A	29840	3	86	
29658	60026	A	29841	1	1481	
29659	60027	A	29842	217	2040	
29660	60028	A	29843	1	132	LNTKSAK*VGGSSRVNVPQVFI SLVSQMFSENDLPLVRKRKTEP
29661	60029	A	29844	115	903	
29662	60030	A	29845	1194	2311	
29663	60031	A	29846	368	502	
29664	60032	A	29847	1156	1359	SEPVYPLCYLRQLAVQANPRR MRCIARHFNINGNRHLTTTINFI *SMVSLIANRLLIIDLIHTVDFY
29665	60033	A	29848	1	228	

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29666	60034	A	29849	102	296	YRNSHNLLQGWOIHRGDLLYH SSPHSR*KHRNRHNARARIPAAI HDNLACVQPTLSAFHQDMCS
29667	60035	A	29850	1	4185	
29668	60036	A	29851	1	906	
29669	60037	A	29852	19	195	GEFDVNIAAVVLPDVA*TPYPA YRRDLIAIGQCVIDQCFLIRV TNPAGSFFELRIHH
29670	60038	A	29853	2	834	
29671	60039	A	29854	2	193	DYAFILQSKRTVALDIKQTGVI QGLPLLFSGNLKVKAIRSGT/H* RCTNATAGGRSYRKR*IRTG
29672	60040	A	29855	1591	3150	
29673	60041	A	29856	2	222	
29674	60042	A	29857	16	359	TTHKTRWQAPVPLRGSPVVAL RIPSDQSEAV/HSLSGVLIALFRT HRFLSGRMFPDHRVWFRMIGSE LVPGYRLSWLSFFNRHYICFTRI RRFRWHRSSLFHGMNVKYRRS KINN
29675	60043	A	29858	207	470	ATIL*GDFYP/GSRNWLGVSSSA IQMAGCVSLPGAGKRCSP*ICW SNWKQTSRTS\GHVLAGSCCW NGKTLRKSDSRWQQLLRRSLIR R
29676	60044	A	29859	3932	4195	
29677	60045	A	29860	4424	4594	LISTPRKKVRT*SFAGLLRISSG VPTCTTSPFCIMAIRSPIRMASR SWEIKTMVR
29678	60046	A	29861	593	1881	
29679	60047	A	29862	3	198	
29680	60048	A	29863	1	1590	
29681	60049	C	29864	1	5421	
29682	60050	A	29865	63	185	LCQSHAPRKFPARPFRRFR*RQD CQTSVFLLRPVANRAPA
29683	60051	A	29866	1	715	
29684	60052	A	29867	1	1212	
29685	60053	A	29868	886	1185	
29686	60054	A	29869	190	433	AFAKLFIMAAALTSGVAHLSSS GTPFRPFCLPSC*LSSSRAAAIST CSLYAAWFPLTLIRCRGIRKSPII CGISRCRCWRQ
29687	60055	A	29870	1	439	
29688	60056	A	29871	14	106	
29689	60057	A	29872	2518	3024	
29690	60058	A	29873	448	537	

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29691	60059	A	29874	463	889	FFGLVTSSPSADSPAMLDTRNV SHTGLGPIIPLTFEAGIHTRPTPN SPPRSCLAPAICA*FFSPAARITT CCASLYRSPLKTLRSVRFWRSS ASVLMRRSSSAAPMPEATLRVL SGLRGRSDKAFTPHPTI*CLEA FPGSRAFVASAP*CLTLRANQR KGCW
29692	60060	A	29875	524	1006	SLLAWLSGINIFASSRIAISPLA ASVPLSMDNISLCTPSGVPEKV TSTVLTSPVQSCKLMMKDFSGP *FP*EKRVSCTSPNCTLICLLSCA STHVLRRNDPLMLTVPSWANS SQPHVNPKNRIQIIPFNITPSLV NQIKIETTRAFTPLLPLCGLITK
29693	60061	A	29876	2005	2517	
29694	60062	A	29877	1	470	MQR RDGDIALIYRSKIGPRTSIT FTARRANPVQRIAARILLRDHLI CRM SCTAARHANTFDLIQSG ADNFAAIYGGANDRITRADA/V SRGCWKLAPVRDIKRQTVAAF YHQDIQPGSCHDQNAL*STGFW REQSGGQ*P*AG*TNSRTRCCIT GR
29695	60063	A	29878	734	1306	
29696	60064	A	29879	743	901	
29697	60065	A	29880	771	1013	RLGTVGTDLSWCYQYQLCYQ* ALPFSTLPAKLAGNGCQRRRCA GTHSLWHADLGSVWPADSLF QRDGRAGGGATRLRR
29698	60066	A	29881	1094	1345	
29699	60067	A	29882	2	751	
29700	60068	A	29883	239	483	PTPQHLYTHALTGSTIMSQRGV DIPCHWHDITCGHAHSLPHRRG RKA*SMGNR*YSCTWCYCEGG TEKAIWPGDGCPGLSV
29701	60069	B	29884	228	803	
29702	60070	A	29885	488	636	
29703	60071	A	29886	1	2117	
29704	60072	A	29887	665	795	

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29705	60073	A	29888	1743	2013	LQCTQYAVGENPAVNFAGRPK GSPCFGPGGGGLIN*AAADIPVAS DNPAHYADAI RYNARTPLQAG VYFVRDGPGLASVRNKERYF ANNYIYDMGRNKDGRQSTWY MGLGTDIDTGLPMSLSMNVYA KYQWQNYGAANENEWDGYRF KIKYFVPITDLWGGQLSYIGFTN FDWGS DLGDDSGNAINGIKTRT NNSIASSHILALNYDHWHSVV ARYWHDGGQWND DAELNFGN GNFNV RSTARGWLPGTICRPDK MRQHRIRHCAPIAGCGTGCRPD KTRQASHQAQMSNAYDYSEIQ PPSEGEILLDAQPLESWSSKAF RKVAYLPQQLPPAEGMTVREL VAIGRYPWHGALALLGAADRE KVEEAISLVGLKPLAHLVDSL SGGEPGVDRMLVAQDSRCLLL DEPTSALDIAHQVDVLSLVHRL SQERGLTVIAVLHDINMAARYC DYLVALRGGEMIAQGTPEIM RGETLEMIYGIPMGILPHPAGA APMNTAHAAAIDPNRIVALEW LPVELLLALGIVPYGVADTINY RLWVSEPPLPDSVIDVGLRTEP NLELLTEMKPSFMVWSAGYGP SPEMLARIAPGRGFNFSVRNTP LARTLQLILREGPRGHPALVQV VDLLIEPPQLPLLVP SVQTRIPRI QPQSHPAHGVNEAVRNPTVWV APFIDEIISIIHKYSI
29706	60074	A	29889	1	1584	
29707	60075	A	29890	1	1188	
29708	60076	A	29891	728	970	
29709	60077	A	29892	2447	2665	
29710	60078	A	29893	255	1360	

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29711	60079	A	29894	1	1890	<p> MYSRFDIVVAEPICTLTTFGKET  VVSDSQTRTTTTDDPLQVLQV  LDRADIRPTHNEDLPFQGGALG  LFGYDLGRRFESLPDIAEQDIVL  PDMAVGIYDWALIVDHQRHTV  SLLSHNDVNARRAWLESQQFSP  QEDFTLTSDWQSNMTREQYGE  KFRQVQEYLHSGDCYQVNLAQ  RFHATYSGDECQAFQLNHGN  RAPFSAFLRLEQGAILKLSPERFI  LCDNSEIQTRPIKGTLPRLDPQ  EDSKQAVKLANS AKDRAENLM  IVDLMRNDIGRVAVAGSVKVP  ELFVVEFPFAVHHLTITAQLPE  QLHASDLLRAAFP GGSITGAPK  VRAMEIIDELEPQRRNAWCG/SI  GYLSFCGNMDTSITIRTLTAING  QIFCSAGGGIVADSQEEAEYQE  TFDKVNRILKQLENYRRALRDL  KEEVAIRLSPFELSAFCSPSIASM  ATRYPNGRHIPDLRLPKERGIII  VFTGNGKGKTTA AFGTATRAV  GHGKKVG VVQFIKGTWPNGER  NLLEPHGVEFQVMATGFTWDT  QNRESDTAACRE VWQHAKRM  LADSSLD MVLLDELT YMVA YD  YLPLEE VVQALNERPHQQTVIIT  GRGCHRDILELADTVSEL RPVK  HAFDAGVKAQIGIDY </p>
29712	60080	A	29895	159	475	<p> VKVNLWPAMLLHSGYADHPYS  RFDIVVAEPICTLT TD/GRCSHIS  LYAAGIINSDSKGAVIMPPIGA  AIRLITSEPAPVPHRIGSRPAIITA  TVIAFGRTTRTAP </p>
29713	60081	B	29896	158	810	
29714	60082	A	29897	1	2070	
29715	60083	A	29898	1081	1218	
29716	60084	A	29899	289	1014	
29717	60085	A	29900	145	297	
29718	60086	A	29901	452	568	
29719	60087	A	29902	21	185	<p> VHDQPSQEIQQRTEAPGAPRSS  RRVAQCHPQPGES*SRAQIPPAS  TPKPGGGDL </p>
29720	60088	A	29903	1	711	
29721	60089	A	29904	2	825	
29722	60090	A	29905	812	961	
29723	60091	C	29906	1	1587	



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29724	60092	A	29907	3	403	LVFDDGDVQMGFWCCGPFCLL VFLLTVRSLSCRSVGV CWRSTR DLVCLGISSGGCRTC VNIAEQQM LLPDCSSGIFVSEGYLAV*GVSL PLLGGASQLGLGSM AIFMILILP IHEHGMFFNL FVSSFILLSSCL
29725	60093	B	29908	168	863	
29726	60094	A	29909	340	612	
29727	60095	A	29910	1	834	
29728	60096	A	29911	92	548	
29729	60097	A	29912	1251	1682	VPVALAAARRSELSRTAAADT G*SAAAELVNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGGQSSWAPFEWEGAPR GEEWTLVSVGALK
29730	60098	A	29913	1	1278	
29731	60099	B	29914	1	2007	
29732	60100	A	29915	406	615	
29733	60101	A	29916	52	391	SNRLLKLMHSSRSCVMFFSSIR SFKDFSLVFDDGDVQMGFWCG CPFCLLSFPF*QSGPSAARSVGV CWRSTPDPVCLGVSSRG CQTV NIAEQQM LLPDRSSGSFVSEGY PAV
29734	60102	A	29917	759	1190	VPVALAAARRSELSRTAAADT G*SAAAELVNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGRRSALGQLSEWQSGQ SPAGAAIAAFDNR
29735	60103	A	29918	84	3661	

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29736	60104	A	29919	1	1230	MDAGWSDVGSWSSLWEISAHT AEGNVCHGDVINHKTENSYYV AESGLVTTVGVKDLVVVQTKD AVLIADRNAVQDVKKVVEQIK ADGRHEHRVHREVYRPWGKY DSIDAGDRYQVKRITVKPGEGL SVQMHHHRAEHVWVVAGTAK VTIDGDIKLLGENESIYIPLGAT HCLNPGKIPLDLIEVRSSTYLE EDDVVRFADRYGRGNDMKKL TCFKAYDIRGKLGEELNEDIAW RIGRAYGEFLPKTIVLGGDVR LTSETLKLALAKGLQDAGVDV LDIGMSGTEEIYFATFHLGVDG GIEVTASHNPM DYNGMKLVRE GARPISGDTGLRDVQRLAEAND FPPVDETKRGYQQINLRDAYV DHLFGYINVKNLTPLKLVINSG NGAAGPV/VDAIEARFKALGAP
29737	60105	A	29920	1	1398	
29738	60106	A	29921	426	1861	
29739	60107	A	29922	863	1388	EPERTSIKSSGIFPGFSRQCVAPS GI*MDVVFTKQFDITINGDFCRS RDNHPVFRAVMVHLYRQALAR FHGDAFHLVAVARVDRVIFAPR TIHFAMHPMLMATIGFDLLDHF FHILYRVTVGNQHRIFGLHHYQ IFHPDGGDQARFSIHIAVFSFVIN HIAVANVALGGVGADLP
29740	60108	A	29923	1	2055	
29741	60109	A	29924	1	2047	
29742	60110	A	29925	1	1294	
29743	60111	A	29926	1	1020	
29744	60112	A	29927	1	1422	
29745	60113	A	29928	1	1698	
29746	60114	A	29929	210	340	YGDVEHESWLSCVRHAHPRIP FA*PTLISLQKRLGKWSGVTGA
29747	60115	A	29930	1230	1404	TFSDCQLRQQPGRNHHHFLWK GYGHHHYRNLP/VPNGPPLSLL P*YCKAKFKPSTSQVP
29748	60116	A	29931	63	281	
29749	60117	A	29932	345	467	LPTRCTYTNLTRRRSPPAWYY* *YWHRDICRSTPARRQTE
29750	60118	A	29933	29	281	MFGKELGRRDVSQLGAAEITYI LKD*T*ES*EILCGGRFLLPLRG RTLQGEWPSLYFHSDCSSHAE QCLLYGFADWAPLAFFR
29751	60119	A	29934	520	714	

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29752	60120	A	29935	222	527	LPSKLASGRCSFCDHWY*SQKS SHSGTLKSKKGQTLTAELGHLI SFHLALLSQHLV*WQDRLQQR ELHSDHWYFSRSSRGSLSPLDIEG DLIQGQRHRDHGP
29753	60121	A	29936	586	837	
29754	60122	A	29937	203	864	NSTKASQA/GRRVLLIDNGKKP GRKILRDPVESSDALFGVPAPA QVASGNRYGYSLNDALNGGD AESAGLTPELWPRHHGHGPA GVKLVEQLCQRLRPNEIRDLA RLVAEFHDLIHTFPM LNPKTIV KLFDSIDAWRKPRVEQLALTS EADVGRGTGFESADYPQGRWL REAW EVAQSVPTKAVVEAGFK GVEIREELTRRRIAAVASWKEQ RCPKPE
29755	60123	A	29938	322	919	VRAVFSLREQIRSHEIRRSAAVS NHQHFRACGHIDRRTVQTLA HLTFRFGDKGVTRPEDFVHFW HRFRTKGDPLLTFWPSAPVTAT ILRIPLANGFRHDHKSSCMTR VPQVPEDPVKSHAPQQFWIHH GKWFAWYDVAIGIPGFAGRS\ CVILLGDAVREVTRVSNAPPAK RYIGGSPRRGFINS CNMPGIISPG
29756	60124	A	29939	1	114	
29757	60125	B	29940	1	4191	
29758	60126	A	29941	512	661	
29759	60127	A	29942	1	1254	
29760	60128	A	29943	247	855	RKKPLP*QRDISSSSLLSLRAFW ASAPVTATNPPDTLGN GFFRHD HKSSCMTRVPQVRSPTELNRSQ GASRPRGVIQQLGHRDPNGDDS HRVRIGLIKHMP
29761	60129	A	29944	1	2313	
29762	60130	A	29945	2	2687	
29763	60131	A	29946	1	936	
29764	60132	A	29947	1	966	
29765	60133	A	29948	1	675	
29766	60134	A	29949	1	792	
29767	60135	A	29950	2	929	
29768	60136	A	29951	1	969	
29769	60137	A	29952	1	420	
29770	60138	A	29953	1	549	
29771	60139	A	29954	1	450	
29772	60140	A	29955	1	606	

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29773	60141	A	29956	1	726	MARGNAITLPVCGRDVVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSFLTGTGQQT AFGRRVSGVIECDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFP\WFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRL
29774	60142	A	29957	1	771	
29775	60143	A	29958	1	1491	
29776	60144	A	29959	145	1929	VSGVIEIADGSRRRKAALTES DYRVLVGELDDQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCALHRIETEL MGKFDEGKLPTDPHMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAELFDYTS LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGNSVLRK
29777	60145	A	29960	1	1731	
29778	60146	B	29961	1	3345	
29779	60147	A	29962	1	1959	

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29780	60148	A	29963	1	1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQVRVGYTIEQI NHMRDVFGTRLRRAEDVFPPV NVSKSDDTLKINGVEDHKTIHD GDGKTYQNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIIELNNDYTLK KVMKPLITSNTCDNLKTCHTSH GSVMAETA VINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICEII VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPE/EDAGDE KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL SETK/EITHPYAMPLYESLCQYS
29781	60149	A	29964	1	1557	
29782	60150	A	29965	1	2259	
29783	60151	A	29966	1	1959	
29784	60152	A	29967	1	2277	
29785	60153	A	29968	1	2418	
29786	60154	A	29969	1	2028	
29787	60155	A	29970	1	1650	
29788	60156	A	29971	1	1170	
29789	60157	A	29972	1	1446	
29790	60158	A	29973	1	1191	
29791	60159	A	29974	22	1893	

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29792	60160	A	29975	1	1375	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KIRRKNGPVSATFTSDGKIRLFY TDYSGKHYGKQSLTTAQCDNL KTCHTSHGSMVAETA VINHKK RKNSPRIVQSN DLTEAAYSLSR DQKRMLYLFVDQIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDGSGIVSL/KIDW/IIE/ RYQLPKVPSPEARKITRRWRIV KQRI*LGFLRLSEMPRKQGDY RTRIWKFE DGLSNVLVIQLNKLI ICVMCLVRDCDVLKTYFHR
29793	60161	A	29976	1458	2675	CDNLKTCHTSHGSMVAETA VI NHKKRKNSPRIVQSN DLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAM/R IPLH*LFR*TLRQTKPDNSAGKC VKI**HTQNQRSGRSQND*RR GI
29794	60162	B	29977	1	1317	
29795	60163	B	29978	78	215	
29796	60164	C	29979	225	422	
29797	60165	A	29980	1	368	MAETA VINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGD/EKGY ESFPWFIKRIYSR
29798	60166	A	29981	1	409	MAETA VINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEKDAGDEKGY ESFPWFIKHSTNITSLSLWFFSS CTH
29799	60167	A	29982	1	814	

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29800	60168	A	29983	3	678	GSVMAETAVINHHKRRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQNRFTQFRL SETKEITNPYAMRLYESLCQYR YSFPPDYFHGLALNVCGFSTRYT VQDVGGSIILGSGGQWLSSHSS SRQCP
29801	60169	A	29984	2	660	
29802	60170	A	29985	179	283	MGQGRNPQTRRTYGCQFRMV K*HGIEMKCEELIL
29803	60171	A	29986	1	643	
29804	60172	A	29987	2	1073	
29805	60173	A	29988	1	1167	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYNV VFALAGSPEDADDTSIYMFYQK CDNLKTCHTSHGSVMAETAVI NHKRRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVV FYRPEEDAGDEKGYESFPWFIK RAHSPSRGFYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAMR LYESLCQYRK\PDGSGIVSLK/ID WIIKRSQLPQSAFYQPFMGLRR ESFYFRWERRTLGPLKSFSV KR GTEAGKFRLAALLVRL
29806	60174	A	29989	1	1692	
29807	60175	A	29990	1	1788	
29808	60176	A	29991	1	960	
29809	60177	A	29992	1	1385	

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29810	60178	A	29993	1	936	MWLVTTTELESTDEHFYHHSK CYWPRAHLGECILSIEAACQAA GGEAGNGGSAVTKATLGSRQG AQHWKALARTIRQEKEIKGIQI GKQEVKLLPFADDMIIYLENST DSSKKLSELCDNLKTCHTSHGS VMAETAVINHKKRKNSPRIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAH\SPFQRAIYS CTICNP*ILIPFSFIGLQNRFTQF R\LSETKEITNPYALRLYQSLC
29811	60179	A	29994	1	1641	
29812	60180	A	29995	1	1551	
29813	60181	B	29996	90	1515	
29814	60182	A	29997	452	1523	
29815	60183	B	29998	9	2021	
29816	60184	A	29999	1	960	
29817	60185	A	30000	1	864	
29818	60186	A	30001	2	917	FLFSPLEMQIQRFTSPSPDIPYRA SSSNCAPRGISPQELTVDLQTKC DNLKTCHTSHGSVMAETAVIN HKKRKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFY RPEEDAGDEKGYESFPWFIKR AHSP\SRGL\YSVHINPYLNSLFY GVQNRFTQFRLNFVQKSRLVD LALKGLRVLLVEGNDPQGTAS MYHGWWPDLHIHAEDTLIPFY LGEKDDVTYAIKPTCWPGLDIIP SCLALHRIETELMGKFDE



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29819	60187	A	30002	1	1756	MPASGNENDLNMPSGTIEIFVR CYVEVERIMDFADFGTTIKQDF RLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLES GHQAPCMKSNNALIVILGTVTL DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDRFGRRPVLLASLLG ATIDYAIMATTPVLWIYPLCDN LKTCHTSHGSMVMAETAVINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFDVQIRKSDGTL QEHGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAM/RIPL H*LFR*TLRQTKPDNSAGKCVK I**HTQNQRSGRSQND*RRPV LASLLGATIDYAIMATTPVLWI YPLCDNLKTCHTSHGSMVMAET AVINHKKRKNSPRIVQSNDLTE AAYSLSRDQKRMLYLFDVQIR KSDGTLQEHGICEIHVAKYAE IFGLTSAEASKDIRQALKSFAGK EVVFYRPEEDAGDEKGYESFP WFIKRAHSPSRGLYSVHINPYLI PFFIGLQNRFTQFRLSETKEITNP YAMQSPYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN
29820	60188	A	30003	1	1653	
29821	60189	A	30004	1	1128	PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRNRERTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGSMVMAETAVINHKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFDVQIRKSDGTLQEH GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLY\SL CQYRAFVNGGGEKARGKPIL CRYGVGM

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29822	60190	A	30005	2974	3878	PSKASELGRKQRRPVLSDSSYA QRKKKYPPWEKLQGSVRGETP VINHKERK\NSPRIVQSNDFPEA AYSLSRDQKRMLYLFVAQIRKS DGTLEHGDGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPW FIKRAHSPSRGLYSVHINPYLIPF FIGLQNRFTQFRLSETKEITNPY AMRLYESLCQYRKPDGSGIVSL KIDWIIERYQLPQSYQRMPDFR RRFLQVCVNEINSRTPMRLSYIE KKKGRQTTHIVFSFRDITSMGFF LESPTQGLASPE
29823	60191	A	30006	233	1538	
29824	60192	A	30007	1	2331	
29825	60193	A	30008	1	1857	MPLRFSSSSRIPYYVNLLHKAA TGFERIDYNFETHSSLEIATDAL TISDHHPCESAAINAETRPSTVL EELARAIRQEKEIKGIQIGKEEV KLSLFADDMIMYLENPKDSSRK LLEWIKESNKVSGYKTHVHKS VALLYTNSDQVENQIRTQPFYN SCENKIKYLAIYLTKESKDLYK RNYKTLLKEITDDTNKWKHIPC SWIVKVAGVESWIHTQVEVW TPPEETAGSTAHSQDQPDQPR YTCEPLEDLHLLFQKETSHTIKA STTDPEEKPLPPYKRYCDNLKT CHTSHGSVMAETA VINHKRKR NSPRIVQSNDLTEAAYSLSRDL KRMLYLFVDHIRKSDGTLEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVHINPYLIPFFIGLQ\NRF TQFRLSETKIPVIIQEAGLSQSEK QAADGIQGVAPAFQVCDGCG SSLQHFFLLMLVDFQLPPLNL RVLIMATLFTIACYVELRGYML HAFQLVSLAMSHLHLAHNQDT HPAISDVLVWCALSHSLEFHRA SDVRADLSNAYSEEVKFGFLL WGLDCASLHRSDFITSSETKYH
29826	60194	A	30009	1	944	
29827	60195	A	30010	1912	1915	
29828	60196	A	30011	1503	1961	

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29829	60197	A	30012	1	6552	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQIRLGDP GSSRLSMEHGLRSIPAWTLDKFI EDYLLPDTTTFGADVKSANVV CDFLKERC
29830	60198	A	30013	1	2679	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALK SFAGKEVVFYRPEEDAGDEKG YESFPWFIKRAHSPSRGLYSVHI NPYLIPFFIGLQNRFTQFRLSET KEITNPYAMRLYESLCQYRKPD GSGIVSLKIDWIIERYQLPKVPS PEARKITRRWRIIVKQRI*LGFL RLSEMPRKQGDYRTRIWKFD GLSNVLVIQLNKLIICVMCLVR DCDVLKTYFHR
29831	60199	A	30014	2641	5798	CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSGHINPYLIPFFIG LQNRFTHFREFMEQKKSPSNRFT QVRLSETKEITNPYAMRLYESL CQYRKPDGSSIVSLKIDWIIERY QLPQSYQRMPDFRRRFLQVCV NEINSRTPMRLSYIEKKKGRQT THIVFSFRDITSMTTG

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29832	60200	A	30015	1734	6267	QQHRNPQKGKQWSYKSTFKFK SESDIHLAEHHKQVLYDGKLAS SIAFTYNAKATDAQLCLESSPK ENASIFVHSPHALMLQILTEQV CTQVVHKPHPEPDSTVKIQNPS EQMAVLYCIVLVGGEFDLEMN FIIQDAESITCMTELLEHCDVTC QAEIWSMFTAILRKSVRNLQTS TEVGLIEQCDNLKTCHTSHGSV MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGL SIVSLAKIDWIERYQLPQSYQR MP\DFRRRFLQDVQNETHGNT
29833	60201	A	30016	1514	6335	
29834	60202	A	30017	2033	4226	
29835	60203	B	30018	1	5670	
29836	60204	A	30019	1968	3130	
29837	60205	A	30020	34	431	
29838	60206	A	30021	320	528	
29839	60207	A	30022	1373	1868	
29840	60208	A	30023	3	1771	
29841	60209	B	30024	1	2299	
29842	60210	A	30025	2	488	
29843	60211	A	30026	1	127	
29844	60212	A	30027	1	812	
29845	60213	A	30028	1	1830	
29846	60214	A	30029	1	836	
29847	60215	A	30030	297	936	RTSSSLMRSSSSLLRICSGVSPRS IPRWFTSVSLPSSFIR\RIITTFRYT PGHVAPASRRSCYKYRR*PMRL YTMIQSL/VGSRPSGLRAFSSD CSPLPRTCSLSRRRVLMITTSRS *SLTYGVDPSVRPVLAASEYF SRR\YAGFQNPNNLLVSG*YQG NYRHFGILRGYPG/TLKNSNFQL TRSARISLSSRSSICTSTGGNTTL PPSSPPDC
29848	60216	A	30031	1818	1991	SPSHIRRTAPNGLRHYQR*IQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPQGW
29849	60217	A	30032	2	501	
29850	60218	A	30033	1419	1640	IFCASLSLGLYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVLPQGC DPHMESLI

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29851	60219	A	30034	1	1593	
29852	60220	A	30035	107	195	
29853	60221	A	30036	1480	1605	TILRITFQFCRSNRRRQRQ*NRF STSQRRCYFLLNGEDVTLTP
29854	60222	A	30037	1	373	MPSYFTSRIA AVHVSALREEQA HHESKHESFIAQRMFRMFYQ ARNLLHAGQENLFSGLTALTAE FTVGEEATRGKTTGKRGPSPDG RILRTTKTRNPRGYMQGRYLES QRDVEATDKPFEFFMNRFRLL AAPRVEFIAYTGLCEDVIRPQL DEAIAQGYLTECADIWQITEH GKLFLNSLLELFLADGYHMR MIGAGAH LAVGIDPTQLFLCQF EAVRKLLGNDQRAHLLPLGIEQ LPALKAFDTVFSMGVLYHRRSP LEHLWQLKDQLVNEGELVLET LVIDGDENTVLVPGDRYAQMR NVYFIPSALALKNLWLKCGFV DIRIADVSVTTTEEQRRTWMV TESLADFLDPHDPGKTVEGYPA PKRAVSDCAQAVKMTNMISYQ GLVRTFLSTSPNNWLVMQNG QEVVIDSGKSVS*RSVCFGCFIK HGICSMRDKKISFLV*RRLLLS LSAKKLHGAKQRAKGDLP RMG AFCVPPKRVIRVVICKEGIWKA SVMSKPQISRLSSL
29855	60223	A	30038	561	845	AKIVQLRPRILRPSRSARRCPSA PRSRQRRRSGPLPEPAPRVS*Q IFPSQYWRYRQSTENQKQRLDP RGQIVNVPARRIIRQKRKCKV AGSA
29856	60224	A	30039	1	1090	
29857	60225	A	30040	1	1384	
29858	60226	A	30041	1	1377	
29859	60227	A	30042	2268	2684	RCRRCKRRLRRFRSLLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRCHCG*RQC SSDGRKITSVHRGRNADGRELT HQA VRLAYLSDRFARHHRHL RNAHRRGPDRIPKERHFPATKL RHTPAV
29860	60228	A	30043	1130	1310	RLDKQNRQGGKRQRNNGVFHQ QPQRR*RTDVIQMPHSHRHA QRRDHQQLGQH HAGRNFE
29861	60229	A	30044	395	689	VAASVSSSMSCAPVLM TVVTR CTLLILSQFMRRKA IKK/LSGSL LPASEVKVLKRDGDYSE/VQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPQGW

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29862	60230	A	30045	1	2142	
29863	60231	A	30046	1	2463	
29864	60232	A	30047	1	1066	
29865	60233	B	30048	790	820	
29866	60234	A	30049	3	126	
29867	60235	A	30050	1853	2257	
29868	60236	A	30051	90	411	
29869	60237	A	30052	1375	3174	
29870	60238	A	30053	5	206	
29871	60239	A	30054	1	1986	
29872	60240	A	30055	339	596	PPYKRRKRRRESVSDGMRNTG KTRRTR*IINLLGRS*NRNFVSV PSGQNY*ISLDHGRENYYGGYS TIQNRLLRLPLSRSGCILQ
29873	60241	A	30056	634	924	
29874	60242	A	30057	42	665	KYGVNPGPYGGTTARKLYEKK LLKLREQGTESRSSTPLPTISSA ENTRQNGSSDSRYSDNEEDSK IELKLEKREPLKGRAKTPVTLK QRRVEHNQSYSQAGITETWTS GSSKGGPLQALTRESTRGSRRT PRKRVETSEHFRIDGPVISESTPI AETIMASSNESLVVNRVTGNFK HASPILPITEFSDIPRRAPKKPLT RAEVG
29875	60243	A	30058	1822	4791	
29876	60244	A	30059	310	1275	
29877	60245	A	30060	52	390	
29878	60246	A	30061	250	1530	
29879	60247	A	30062	1	1641	
29880	60248	A	30063	1009	1140	
29881	60249	A	30064	913	1218	
29882	60250	A	30065	900	999	
29883	60251	A	30066	2282	2741	
29884	60252	A	30067	1	2199	
29885	60253	A	30068	1	2229	
29886	60254	A	30069	441	608	
29887	60255	A	30070	122	517	CTIVIRSRCFWWKTAWAQKMN LLPMARLTTTIALATYANISAQ WAKRLQTAFR*WATPHGAVLI *FPALRVK*ANATALLTVTT QATGRLRARQRKTATPRTIRPG ESTSSSPRSSGSLAPACSVPM

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29888	60256	A	30071	498	1155	KOPSAVSGTGAAGEANLHAVR TAEQTAVVYRHRQRVRYLLR YGILDWSPTYLKEVKHFALDKS SWAYFLYEYAGIPGTLLCGWM SDKVFRGNRGATGVFFMTLVTI ATIVYWMNPAGNPVDMICMI VIGFLIYGPVMLIGLHALELAPK KAAGTAAGFTGLFGYLGGSSVA ASAIVGYTVDFFGWDVGFMLS HELWESEFTKLKYEYNNSCPAS VSGWL
29889	60257	A	30072	670	1100	NCRKTSPKRRFSFDDPKSDRAK DFLAKILH*SLWRAYPIARHLTL YRFAPRICYILALPLSQRSTQQG ATMALPILLDCDPGHDDAIAIV LALASPELDVKAITSSAGNQTP EKTLRNVLRMLTLLNRTDIPVA GGRGKTVNA
29890	60258	B	30073	861	935	
29891	60259	A	30074	1	2510	
29892	60260	A	30075	3	119	NALRKSASSCSGRNRYPGS*PS RPDCQRSCSHKHAGYG
29893	60261	A	30076	3	227	GGEGRASCSADTGWLPSDPPGC AAGALGGGGWAVAGAAAGGP CA*SAGGIGVHAPKAQHPATFS GPAEGVIPPQ
29894	60262	A	30077	1	2277	
29895	60263	A	30078	1	2187	
29896	60264	A	30079	1	3666	
29897	60265	A	30080	1	699	
29898	60266	A	30081	513	1019	TGGVCCWCARYVDALVVFAD QLFVAEVLASAHSPSRLYAHAH GDTPQRLRLNGRQALSP*FCCN HRAALQRHQPVRLPARQSRQ MRRCNLLYQKASAQRSQRDSS *RSLFFRSVDADGG*R*SHGYA FRHGRFQCHRPGLPGTGPPRH ADSAFSRRLIYPACRWRL
29899	60267	A	30082	389	462	
29900	60268	A	30083	1	278	MGVNDAVLEMHGLGNDFMVV DAGFDQLLVVEPPYDLELDFHY RMFNADGS/DSGAVRQRCALLC PFCASERTDQ*A*YPRQHRQRA DGSDRHR
29901	60269	A	30084	1240	4914	
29902	60270	A	30085	1	1308	
29903	60271	A	30086	30	164	VTWW*RAPTAGLMQC*YCRNR RARLRLTYGHAPAHRRNGPDV PS

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29904	60272	A	30087	3	264	TLRPANRF*HIPDAAGVIPVGY AL*RGTSVSAVHRW/CSTVFGV NWTATLATKLMVAGIRRS GAAS RISRASPPSFSVPACSVGRKKVI
29905	60273	A	30088	1	3639	
29906	60274	A	30089	1	957	MGFRRTMPHIVISALVGGLLV FADCLAWTCRHKLDLDDISDA KITGLTSKAIRFYEEKGLVTPPM RSENGYRTYTQQHLNELTLLRQ ARQVGFNLEESGELVNLFNDPQ RHSADVKKRRTLEKVAEIERHIE ELQSMRDQLLALANACPGDDS ADCPHENLSCCHHRAGKYVG LIRRVKRRIRHRCWPIKTL SQRA VSEFQRLIQPNHQYQSYTROCA PETDNHADNSYNAGLFIVNSLY TAEGVMDKHSLWQRYVPLMR HEALRLQVRLPASVELDLLQA GGIGLLNAVERYDALQGTAFTT YAVQRIR\GAMLD
29907	60275	A	30090	1	699	
29908	60276	A	30091	430	660	HQTHFIVEHRRIMQRTARQNIG RHYQIQLSAVQRIRGAMLDLR SRDWVPRSIRRNAREVAQAIGQ MSLPMLQVALS
29909	60277	B	30092	1	1575	
29910	60278	A	30093	1	289	MISANRPIINLDLRLTFVAVA DLNTFAAAAAAVCRTQSAVSQ QMRLEQPLGKNCSLVT VATN C*LNMAFNFLVTPGKSCVLMM RSCIQPNSD
29911	60279	A	30094	1	1095	
29912	60280	A	30095	1037	1297	LILRCPWSYSRCIRILIAPSSS*Q TEAKPFASRASRTSDDCQWANI SSVMPVKPNSTTPSILRRFSTPK CSATNCGEN*LSIMIGS
29913	60281	A	30096	905	2042	
29914	60282	A	30097	87	760	
29915	60283	A	30098	1	2793	
29916	60284	A	30099	308	485	KSLNAICYRNTRTSMACY*PA* VRWPKHSAGLMTISPVLHVISP RHRWLECATRVGRLG
29917	60285	A	30100	1	2784	
29918	60286	A	30101	453	1975	
29919	60287	A	30102	3	470	
29920	60288	A	30103	1447	1773	QFAFTEHHQTQEHHHQRSYDC PQRDPRHIDAQVSDQRPCPSG LREPLHCAQPDGG*ADNSADH IRRNGGDGAFQRKRNR TLDPH KRQEHGGLTLRIKLSVEQAFAG
29921	60289	A	30104	1	449	



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29922	60290	A	30105	188	1508	
29923	60291	A	30106	171	410	
29924	60292	A	30107	3080	3232	
29925	60293	A	30108	1	1272	
29926	60294	A	30109	438	617	
29927	60295	A	30110	259	392	
29928	60296	A	30111	905	1545	RLTTPSLVCWRPAAKRPI LPRS LKQLKKIASRKVTP*/SLGNAW NNLEKQRAYLSMMAQKRVDG LLVMCSEYPELLAMLEEYRIH PMVMDWGEAKADFTDAVID NAFEGGYMAGRYLIERGHREIG VIPGPLERNTGAGPPCRFYEGD GRSDDQVDGDIQFFSTNTTIGR GHFRTMVDGICPKDGNLRFN RILEHREPFYPQIPATFAYA
29929	60297	A	30112	3	466	AIVKFKRNVHQDGGYCSVQIQ QCRFALIFKDFCRMHRHNLIRR TISQQSVGRIRCVSIASGRVYYC FFALEGKKPSSSISAAPTQMAVS ARLKVAKCQSPT*KSIISTTKPC HRRSNRLPSAPPIISATRVHRQM RYSTSSGAAALLSITVTPS
29930	60298	A	30113	1	1562	
29931	60299	A	30114	706	857	PMRELISKGVSPFAISNSGLITS LLTSVV*IDAIDGIRFSFLSWAS GKGP
29932	60300	A	30115	966	1142	SLEETEKYRNVNEMCFPVKRR RREREKTSERTPAPV*VKITTRK LYPAEERTGRIFEA
29933	60301	A	30116	1	3095	MDKFLNTYTLPRLNREEVESLN RPVTASGLEVIINSLPIKKSPGPD GFTAAFYQRYKEDAGEREGEG GNQQVAVRGKRKTTERKKKLG EDVKVKESKNSGAYEVKQHRF FRSLDWNSLLRQKAEIFPQLESE DDTSYFDTRSEKYHHMETEEE DDTNDEDFNVEIRQFSSCSHRFS KAAEVSTRLLSTRVTEIEGWLI VQRNQKLLQSNLKQRSGEPLIL DDDSHVPELRLAGYRLLKNAG CLPPELEQRREAIQ
29934	60302	A	30117	1	2583	
29935	60303	A	30118	1	3141	

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29936	60304	A	30119	1	1037	MRVVILGSGVVGVASAWYLNQ AGHEVTVIDREPGAALSAAN AGQISPGYAAPWAAPGVPLKAI KWMFQRHAPLAVRLDGTQFQL KWMWQMLRNCDTSHYMENK GRCFELPVAVYAGGQAVLVKQ CKAIGGPDRAPTLTNTMPIFKA CTPDNRRAVWRHRAQTSPEER LLDMTAAWIEIANHHLQRFTR LQQLGIKTNNLRHSGKTNAVIV YMIQSISLVDEMSCHLVLTGG TGPARRDVTDPATLAVADREM PGFGEQMRQISLHFVPTAILSQ VGVIRKQALILNLPQGPKSIKET LEGVKDA/EGVPYCIQLLEGPY VETAPEVVAAFRPKSARRDVSE
29937	60305	A	30120	96	711	
29938	60306	C	30121	128	628	
29939	60307	A	30122	1024	1128	
29940	60308	A	30123	193	372	IQTESNPQDIL*NPSPPVFISKHS PNNSYCYAQSREKNKSHFHV ATTENRALSIIWYLMN
29941	60309	C	30124	202	321	
29942	60310	C	30125	150	491	
29943	60311	A	30126	1163	1257	
29944	60312	A	30127	929	1023	
29945	60313	A	30128	3	765	TARAWLLLGPVWPCVSRWSK KPSPRGGRDPSDRDPAFAARS TVPPRISAYERPVWPGEWNP RGPGRRASAVVSPREGNWGVL RDPRLQARKPRMVRSRQMCNT NMSVPTDGA\TTTSQIPASEQET LVRQESSEDYSQP\*LLVALFIAA KKM*KSLKGKKPKTKKRVWN LVCPLMPLNLV*FVKVDLKMV ALSMKQDILWPALH/DAKKL KKRNKPCPVCQRQ/HNSNDCANL FPLVDLSIRELYISNYITLGI
29946	60314	A	30129	2	430	
29947	60315	A	30130	3	1088	
29948	60316	A	30131	303	529	GTGQCANTKMSVPTDGA\TTTS QIPS/SPEQETRVR\PKPLL/LKLL KSVG\AQKDTYYYGKRFLNLG QYIYGLNDYY
29949	60317	A	30132	3	619	
29950	60318	A	30133	123	385	

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29951	60319	A	30134	66	413	HQSEQMYQSSESCLLGTTAKA RGHQLRTASACHFPSTPPFWSL TLESQREGRFKOPTLISCF/CLF MSVPVVSAPPFSSSSSSSSSSSS SRPWFPDQEAR*LTSPVERPCR GLRPA
29952	60320	A	30135	257	465	VPTSPASLESKQSCPHVLCPVW EVEGHVS*TGKPDRPPRRKLLT LLLVPVWVPGQLAIKQEGQEPK KRH
29953	60321	A	30136	1564	1857	
29954	60322	A	30137	33	265	
29955	60323	A	30138	114	560	
29956	60324	B	30139	70	555	
29957	60325	A	30140	650	1045	
29958	60326	A	30141	374	575	
29959	60327	A	30142	1	1095	
29960	60328	A	30143	1	981	
29961	60329	A	30144	28	698	TACRIRHGHAGRLCCSPCLLVIP LKSSQHILRVLNPPNLDGRRKI A\FAHHC PFKGVGRRYA\HVVL RKAD\IDLTKEGGENSLEDEVE RVITH/ILQNPRQYK\IPDWFLN KTRRM*KDGTYSPPG*PIGLGQ QAPVKDLGAD*KKIRAH*/RGL RHFLGAFRVRGQAHQEPLGRR GRHPSGVSKEEIRSVGPCLVNKI VYIPKKKKKKKVDAANLVV VVVVGGR
29962	60330	A	30145	107	340	
29963	60331	A	30146	428	934	
29964	60332	A	30147	1	1533	
29965	60333	B	30148	1	2652	
29966	60334	A	30149	205	450	
29967	60335	A	30150	1	879	
29968	60336	A	30151	139	1029	
29969	60337	A	30152	237	422	WFETPAQYTNRSPESGTHYRRA RSRARWHGCMCVCRRRKSPR ANKPRRLPPVR*RCPPRA
29970	60338	A	30153	1	1134	
29971	60339	A	30154	136	411	
29972	60340	A	30155	1	3345	
29973	60341	A	30156	194	475	TPATVRRGW RPAVRVFRWWK PLTVPPRRKGPLSRGTGCRPVPL TTPSTGTVMRAGICAVKMLIVQ KSPCMPPC*HRQWTMTGLWQA PAAIRPV
29974	60342	A	30157	1	2988	
29975	60343	C	30158	1	3939	
29976	60344	A	30159	308	749	
29977	60345	A	30160	1	1338	

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29978	60346	A	30161	1	4342	MTRDNPVIPRFIHRREVVFIGQE NGGIQNARFIAALFFQHGVNLC QRVGGLLKIGVEVFRYTSVVE RVVVDYYIRPAGFSIDTNDRGS VTDDFAPDGQLAKAIPGFKPRE PQRQMAVAVTQAIEKGQPLVV EAGTGTGKTYAYLAPALRAKK KVIISTGSKALQDQLYSRDLPTV SKALKYTGNVALLKGRSNYL LERLEQQALAGGDLVPQILSDV ILLRSWSNQTVGDISTCVSVA EDSQAWPLVTSTND
29979	60347	A	30162	1	1023	
29980	60348	A	30163	1	679	MFRVTWSSGRTGLGKRLFRTP YDNDGTGPYAFNKTHPKDNYT CTVLFIDDMASGQSLDKAQD NYRQAMKKLSSGRGNVLAQAE AFRGLGVEIKREINPDLAEQAIR LQDCVFDTQETMTTFTGTVSS ANSGNYTIFNTDTGAAFNNVS LAIGNYVVLAFSAS/VGA/DMK MVNSTITASGSKRSTTVLRQGL SQRWLLSAGARNLLQHYSFRE TCANWNMLFIGR
29981	60349	A	30164	114	685	
29982	60350	A	30165	1	1353	

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29983	60351	A	30166	1	1661	MRGEVLLAGVPRHVAEREIATL AGSFSLEHQNIHNLPRDQGGPN TVSLEVESENITERFFVVGKRV SAEVVAAQLVKEVKRYLASTA AVGEYLADQLVLPALAGAGE FTVAHPSCHLLTNIAVVERFLP VRFSLIETDGVTRQLLGVSRYL AMGHAFLIQIADMRNDGGWR DFQFSGNLVMDEPNRSAQTYIK LVKSRLGTTKRYNHKDDCPRC RWIAAMIDNPPRIRKPTKSASV WHATATSASPERQMSTTVIMS ARFISCVWMTFPCMPRSGPMRF VHLPCRFRDAFNTGVGKLDQL GPSMSTRIRQRFTTLCPTLSSS STEFENVSDCRPSRARSCLRFRL CRSIRCVYRLADYVQRSLQAGF IQRPAIRHPYHHVKGAFTEYVR NNRLPETVIRVLQPALARFSPDI APLFSPFPLHDDDV TARLYAPS LMPKLRLIGLTLALSATAVSH AEETRYVSDDELNTWVRSGPGD HYRLVGTVNAGEEVTLTQTD NTNYAQVKDSSGRTAWI/HVET T*H*AKPALPCARSGKSGQNP R*THQYR
29984	60352	A	30167	254	496	RASRLKTCGDGCCSLSAVVS ASPFASRVKSSRRWV*S*VG WPPGMSL*TAEIRRSRRIPV VSSGSLTASFANVVR
29985	60353	A	30168	1	984	
29986	60354	A	30169	1	429	
29987	60355	A	30170	1	523	
29988	60356	A	30171	1	702	
29989	60357	A	30172	302	421	
29990	60358	A	30173	308	2468	
29991	60359	A	30174	612	671	
29992	60360	C	30175	1	2649	
29993	60361	A	30176	501	754	
29994	60362	A	30177	1030	1327	
29995	60363	A	30178	3	108	

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29996	60364	A	30179	404	1347	DVTILARAVLQALLKILYH/KCE FNDEMLTEGVIREKMGFNPQTL REVLQACQQQGCVANLDDLVDV VMIIDGAFSGIVQNWLMNMA GYDLYKQAPALVDNRTGMER ASNGGPWQVQSLPARSYRQLD SYYGEAMAIGERALVALLDFSG PSPSGDWRYQTHHTFPPTGWR RQATLVKMRACIEAVKAVGEE LCPALGLTIPVGKDSMSMKTR WQEGNEEREMTSPLSLVISAF RVEDVRHTITPQLSTEDNALLI DLGKGNNALGATALAQVYRQL GDKPADVRDVAQLKGFYDAIQ ALVAQRKLLAYHDLRI
29997	60365	A	30180	494	1433	
29998	60366	A	30181	1092	1347	
29999	60367	A	30182	315	600	STPIEKTVSKAFSAGSCSILT VTNARASARSACIISITA AVSGSCA PTP*EVSSAFARSLICRSIRKPGL KLRSITIGALASKTVLPASPPRIA
30000	60368	A	30183	535	661	
30001	60369	A	30184	1	1491	
30002	60370	A	30185	1400	1852	
30003	60371	A	30186	199	534	
30004	60372	A	30187	2	539	
30005	60373	A	30188	1	690	
30006	60374	A	30189	127	939	
30007	60375	A	30190	1	665	
30008	60376	A	30191	1287	1548	SSCVLVRWRETADCRWRKLCL TDERTRR\NNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERS DEIPEAAKEIMREMGINPETWE Y
30009	60377	A	30192	242	709	NYMHYHADRCITRCHGNACTV NYAGLRVPTSTVWTGLNLLT KRIKYLMAEWSGE/YISGPCVEP GKKSDQSKKITVSIPLKVLKILT DERTRRQVNNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERT AEIPEAAKREHA*HGGLTPET WEY
30010	60378	A	30193	1	897	
30011	60379	A	30194	1030	1263	
30012	60380	A	30195	263	514	PAHFSVAHSHLWQNINPLSSVQ CRQNHQAIPCRIFELLNVMRH/ VTRDSSSGLGCSWRLTASVNAR RFVDPVQILVMAMSGRRSR
30013	60381	A	30196	1	1995	
30014	60382	A	30197	141	229	

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30015	60383	A	30198	1	702	
30016	60384	A	30199	36	144	DGLLMDERNISPLLQKRMP* QAV*VWWWKDYGV
30017	60385	A	30200	462	646	QWVPIARPMPACHVQRRTSSL ERRQPVMLMVMLRILWYIYCSI HVLG*WICRLYYKTLLK
30018	60386	A	30201	107	1200	
30019	60387	A	30202	366	500	
30020	60388	A	30203	1	1193	LADCSRYNGLEMTLSCCAGAS TDAVGGIERGGLKSPEASEGEI APRLLDGEPLALSGDKWRISP WLLVTDDTATITAFQMIEGK AITLRDGDQTISLSGLKAALLFI DAQQKRVGSETAWIKKGDEPP LSVPPAPALKEVAVVNPTPTPL SLEERNDLLDYGNWRMNGLR SLDPLRREVNVTALTDDKALM MISSQIFNGHMHVHIKDLVFTDH APDKGISFGSDTGMDRPARGD HRLVMHHDMTFLRLPHHVE NAGVIIHIEIEINFHPALVGVRH GVPLVTRSQRQPHTRLAGFQY IRDQIFVNRTVTGEEIAYAEF TNFPANGNRFSYRHNAANNNS VNVAVNHGVLIGDKYLFNQKFI AQPLGIQRFVTRTVDALSYVHI
30021	60389	A	30204	3	1057	
30022	60390	A	30205	1	955	
30023	60391	A	30206	1281	1370	
30024	60392	B	30207	1	2199	
30025	60393	A	30208	1	589	MLKKREQTVFTHEKSVFQGLD RGNRELGPPTFGVKGAQKGN LQIFSEDKNFGPGSGEIWGHR GPKWDIPRGKRETLGKPHFFW KPSQEFGRKGLGSFGPWVERVSG NKNSGKRIYPWGPVDGINCRW REPRNVDVAEYRRDCGSRFRSL RHFYRSLFSLHRPASTRHQKAQ SSAVTVLQTN AQHGRRQRWQ
30026	60394	A	30209	1118	1460	FQASTTQPRTPCAPLSSVWRCR PPRSPWPASWRSVPSSMGLRR TPWCPELLSSRGSTGFLWAEMT SSQARPKSSPCLWTSSLAPASRP CPS*VLQPPGQQRWGEPIGAIAV PL

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30027	60395	A	30210	61	641	RHKHRRRIPGRWDQIRPAPNR WQTGFQWFALPVTGVRLLISGY TELLPRL/PAQKNLPYTIHPAWR FVAHQGRESALECRYVPLPVRH *RNCRWREPRNVDVAEYRRDC GSRFRSLRHFYRSLFSLHRPAST RHPGAQTGAVTGFADEC PARK AAALAKASVNVVVFHSTNATV CHRPDRSRASGSFRRYWRQE
30028	60396	A	30211	214	462	
30029	60397	A	30212	116	283	KKIKRHSLSVINSLANSKNKRR WRKNIKLR*SSLLK*TESPLMA ILVLTSLTAI
30030	60398	A	30213	451	834	IWTGKKVDSARALIARGWGLH VILRRTDDWMDGRRSRHTDDT DVLLRIHHVIGELPTYGYRRVW ASSQTGRT**FKVQNRYPFPVLS DFEHLQEPYEFYFGKLR*PWLPA TGEFHAIEYRSVDFCKHPV
30031	60399	A	30214	1180	2547	
30032	60400	A	30215	341	505	
30033	60401	A	30216	293	4221	KPFSPCCRKGRWLFNRNHSSARR PTVLYYRRSTMR*NSW*PNLRR QRGNPANRS/RQSMLELSGVKD GELIPAKLFNHLVTWLQARQTL SQQNTPRPGGGEIPWCSSVLA ESERKKRGRKKQRGIDSPDVGA LLLVRATFYIWQQPPVNKIALGI EYAASKYYGWQRQNEVRSVQ EKLEKALSQVANEPITVFCAGR TDAGVHGTGQVVHFETTALRK DAAWTLGVNANLPGDIAVRW VKTVPDDFHARFSATAR
30034	60402	A	30217	1	1362	
30035	60403	A	30218	1	1440	
30036	60404	A	30219	389	503	YESARLSGLHRQSDDRWR*SP QYARHTRKRTSAGCSA
30037	60405	A	30220	1160	2385	
30038	60406	A	30221	290	373	
30039	60407	A	30222	1	627	
30040	60408	A	30223	3	862	
30041	60409	A	30224	1	469	
30042	60410	A	30225	241	615	
30043	60411	A	30226	1	1428	



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30044	60412	A	30227	862	1453	SFLLVSPSQACHHYYAP/KIFDL/SGYTSTTEQMWTIVGLTNV/LATFIAIGLVDRGLGFLAMPAGM/GVLGTMMHIGIHSPSAQYFAIA/MLLMFIVGFAMSAGPLIWVLCSEIQPLKGRDFGITCSTATNWIAN/MIVGATFLTMLNTLGNANTFW/VYAALNVLFILLTLWLVPETKH/VSLEHI/ERNLMKGRKLREIGAH/D
30045	60413	A	30228	1	987	
30046	60414	A	30229	767	1472	CMSRQCCTAYVPPVRSCPPVSVHFFFHSRLCRDALNEAFHPSGFQVVKCCDIARIHRNRYGDLLFAIGVVHIANVNAIHRNATFHQRQEIGGCFTNQDFLSIGGAMNVVDNFLQRPETYGDPFCQYHFHQVLLYRIFGNLIVGYQHQCPRKSDPLNADLTVNQAFINPA*NNIWHSVFLFVLLIGLHRLCGMRQDVLNMVDNEFPWRWLQLAGANFHVLRQILADQRQRNW
30047	60415	A	30230	2553	3845	
30048	60416	A	30231	1	656	
30049	60417	A	30232	3	228	
30050	60418	A	30233	185	206	ATVDPPFITEPGDILAGGFA*PLSWFAGFALEHHNLPWATGDLHSLRA
30051	60419	A	30234	12	155	
30052	60420	A	30235	698	2684	
30053	60421	A	30236	1	2004	
30054	60422	A	30237	1	811	
30055	60423	B	30238	1	7521	
30056	60424	B	30239	52	1023	
30057	60425	A	30240	2	163	LTPTWWRKPWNRPVLSVIP*KWKLKGPVALKTA YPAKRLPLPITSFSLPGVA
30058	60426	A	30241	1	2067	
30059	60427	B	30242	1	2787	
30060	60428	A	30243	101	947	
30061	60429	A	30244	1	1917	
30062	60430	A	30245	239	469	KRVSISSRRRFS AQKASASALARWWRSA VNIYVFAI*TTAQRV*QLRMTNCVVRTTITACHSR*RITLSLSPVKPAS
30063	60431	A	30246	1	4348	
30064	60432	A	30247	1141	2244	
30065	60433	A	30248	503	649	

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30066	60434	A	30249	418	930	PRVIENFLFQLTFLPGGITQSHQ YVRRLFIGAERFQHIAGSGHYR VV*NANAGSKIGGRSMQNKPAI FSQRTAEHNRFIQTD*FITRLRR DLQLFQNPFNFEIFQRLVDDDP HCTIGIMFANVDHGTTENRIRK LCFNLNTGTGTQRKGHANISGPE TFRIYHRNAHAPLTI
30067	60435	A	30250	1	526	
30068	60436	A	30251	442	684	
30069	60437	A	30252	1	3144	
30070	60438	A	30253	59	340	LLPQRQAKAPVLPLPLPTENVP AARAGKKDAVIFSSAQFEQIAL AANGAFTGG*YQNRQ*NMRCY ASGESVTDRPRLAIRDATIGISG FCSLA
30071	60439	A	30254	62	298	
30072	60440	A	30255	904	1530	
30073	60441	A	30256	701	1329	HRLSMCRGRCSRWWWSARTNVI SMLVFALSFASWRIVSPRTM/D ALTFAAESALPGSPHISTDHQG QFVFGVSYNAGNVSVTRLEDG LTMLHEELSSHMMKEEQILFPM IKQGMGSQAMGPISVMESEHD EAGELLEVIKHTTNNVTTPPEA CTTNKQPAQPQRDKPQRGNQQ RLASVIFQCQQHDHEHKERHTY PAHQLAERHLVDRLLM
30074	60442	A	30257	8	382	
30075	60443	B	30258	1	2655	
30076	60444	A	30259	67	231	
30077	60445	A	30260	1109	1531	TFLHSIPAAKTQGPPRNTLVDT PQHL*HQQRRTROPQLALSLRT *VFLNRILRGALFAPKACLPD LVISPRGPPQGLGVTRVQVSAH TNPRTTHRNTPHYTRNTQTRPE STPRRDTTTPQQRHTPPHTGK RRGTPET
30078	60446	A	30261	1025	1252	SSTVFSNLDRSDSPISQSKMKIIA SITTIRMED*AIATPYSPSSTRLR M*AVATRVSGVTRNTMALTVV MARTKL
30079	60447	A	30262	2114	2380	LPGLAKLTVKDLPRLSLAFERE VRDSPISQSKMKIIASITTIRMED *AIATPYSPSSTRLRM*AVATRV SGVTRNTMALTVVMARTKL
30080	60448	A	30263	3026	3217	LPQCKWDPYGVITISPVVSIRS ANPSCSTSPFFV*SATKGLLYQQ TRIPALDIPPSSNRRNSHG

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30081	60449	A	30264	1403	1799	YGHEWRWMPGNRPHYGRWPQ HDFPPFKLRPQSVTSRIQPGSD VIVCAEMDEQWGYVGAKSQR RWLFYAYDSLRTVVAHVFG RSLFTGP*RERFATQIEVGKLF AAVDMVLWLSGKAQPDVVV KVVVL
30082	60450	A	30265	3174	4135	
30083	60451	A	30266	1	2771	
30084	60452	A	30267	1	1281	
30085	60453	A	30268	10	233	LRIQASDPEINSRRESGIHLPYTT DKAPSPLTVDGAK*EVSRSI/R QNSQVQHPPDAAKYPSGCHK FRGFRRA
30086	60454	A	30269	300	564	SANSTLKRTQVNRRLTVKLSA RKLPMLKVNRNSLVVVSMV MLLSTCTRWSRVQTRKATSSST TLKV*SLANTSRLIKVSRNS
30087	60455	A	30270	5259	8003	
30088	60456	A	30271	1	819	
30089	60457	A	30272	1173	1369	
30090	60458	A	30273	1	4767	
30091	60459	A	30274	905	1162	FSSVVMCSSIIVSEQEITSRLKAT VASQVADSAGLNSRKITSCRSS AFLSALIRHPTGGIFNKL*LSGT LNPALLSFITSHGILL
30092	60460	A	30275	1164	1582	
30093	60461	A	30276	1	1785	
30094	60462	A	30277	1	168	LEHLSPCDSIRHSRTRATAAIRS RCYSKYAQ*IRDHRVNGDGV RLYAANQHRTCQ
30095	60463	B	30278	1	954	
30096	60464	A	30279	108	530	SIRQTHVQIVRRSCLAIRHQVPS TAIRVGIVKGNFAS*AGAQPSK TLR*HRCCTTRALTSGVLAVRLS AGCNFPELVHRRLTLWRAGRT YPPASGHHHDNRNAPSLSDQTR TDPPIRAHASRYQRQKPDWLT PFPAGQRC
30097	60465	A	30280	1	1389	
30098	60466	A	30281	1	380	
30099	60467	A	30282	1	3255	
30100	60468	A	30283	569	2547	
30101	60469	A	30284	1	585	
30102	60470	A	30285	1376	1693	CPMADTPAT*PIPKRLMLCYST GLPACYITVKPP*TLGSVQGS LG PSSGPKTAGAPSSRPPSPSARRP RTTETRWTLRLSKDYWLITRKV GLGNLQDGGGRAGSLS

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30103	60471	A	30286	737	1088	NMLMNV CNLPVVCVPMMSRK RGCVTITWALICGLSWGCRMS GGLRKPAPRPQKWRCLPIIVGR RKSGGSKIRANVCSLPFPGIIG R*TTGESKRLCRSYHDAAGNDS *WRDLVIG
30104	60472	A	30287	3	209	VQHSCRMCGTHSQKCPSHRQK LRPHGHLVA*CLCAGSREWEA NPLFPGRGHCTDSPPETRPHQL VQRV
30105	60473	A	30288	2366	2768	STRSGGNCRGAGAGV*SGPVA GR*SQSGDRAESTSPLAMVGD GINDAPAMKAAAIGIAMSGT DVALETADAALTHNHLRGLVQ MIELARATHANIRQNITIALGLK GIFLVTTLLGMTGLWLAVLAD TGATVL
30106	60474	A	30289	714	881	
30107	60475	A	30290	791	1618	NTISIRPIKLRS*L/CDPGFAGQPF IPEMLDKLAELKAWREREGLE YEIEVDGSCNQATYEKLMAAG ADVFI VGTSGLFNHAENIDEAW RVMTAQILA AKSEQWGQQVY AIVQNTDQAQAVMPYGPCKLY VLAQNDALQRTENYAESIAALL KDKHPAMLLLAATKRVLFAIV DTYVTTNASLAGIALNSMDLSP GGRVAVKESNQRWCSDFEFC CDNGERL RVTFALDCCDREAL HWAVTTGGFNSETVQDVMLG AVETPLRQRSSVSVSSGVADG
30108	60476	A	30291	364	1305	
30109	60477	A	30292	105	609	CGGCPQSRHRPAPALRYPQLQ MPHWRRSIC TSLHRQR*WTPSG SV
30110	60478	A	30293	159	438	CASVPRSRGGSQAIAARKSGRA LIK SASLS*FK*LLKPAINAG*Q AS*WRASASKPCSASPCAGDN CASIVSAASALALGCSKRISAPR TAP
30111	60479	A	30294	1246	1300	
30112	60480	C	30295	1	1374	
30113	60481	A	30296	231	413	SPRCTRPCNAGSDVRRGSASF* AGGAGY*TPRPGVW*SVGYGE RQQRAPPADWSQRCGVD
30114	60482	B	30297	1	3081	
30115	60483	A	30298	345	505	TNAACNRQSGLINQWMKQTVK ME/VTASGTVISVINPVATKLRR *RVFPAPCCG

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30116	60484	A	30299	3	421	QRRATGDLRLPTR*TARRGGRCDS*SSRRWHRAFTGACREISRQ QNRHRQRPAAGVALVGSE*T SGILAGQRHYRVYRAGYRRSPP AGYAPD*SD*RPVDGRHECGRR PVWRRENVPATGGQIGARHET GGGLPRTVY
30117	60485	A	30300	1	3202	
30118	60486	A	30301	317	554	
30119	60487	A	30302	474	599	TTSVQRTFLPDY*APTPVLLPA RKATAARKLHRFSGRQDR
30120	60488	A	30303	212	569	TSLKVVTALRSMPSPINNLS KVKCSKAFSASCP*NEADFLRN VPPGIRIVCSLSSSDSALTICKLL VITVMLLKRESRGITCKTVLPAS RMIESPSWIKLTAASAISFLWV LMSVL
30121	60489	A	30304	1	160	WSKMSRAVRPSDWESWTQTRE VVRQTVRCRPPPSAAVCLTAS SPANCGIPG**MLAEILA*RAV RPSDWESWTQTREVVVRQTVRC RPDPPSAAVCLTASSPANCGIP G
30122	60490	A	30305	1	975	
30123	60491	A	30306	1	762	
30124	60492	A	30307	1	733	
30125	60493	A	30308	493	948	LGAIFLAGALFAAAWLADFRL GLGARLYRYGADWFCADGGM SAEELKFISENGAVVDMDIKKP GSAAASGPKLHYIKQLLSNRM MLGVFFGQYFINTITWFFLTWF PIYIGNVVSDNR*YVAQITFITW IKTYGRCPSPQRDGDGFVNRCL

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30126	60494	A	30309	153	2031	RRNYQRQQKKRGSEGAGRPDR RSRISAAAYSPRSEFNNAVTEH Y*NRF*T/LVPRSR/HANADTVT REAVNQVIALLD SGALRVAEKI DGLPTNQMQASRRAKEEEVHL TGQPSRVQSPRRCEEKQYMV MIVSGRSGSGKSVALRALED GFYCVDNLPVVLLPDLARTLA DREISAAVSIDVRNMPESPEIFE QAMSNLPDAFSPQLFLDADR TLIRRYSDTRRLHPLSSKNLSLE SAIDKESDLLEPLHGFDPDYDTV GFSCRRRIDYVCRIKHSRRIRQV VLLNFAKSGAFSTTRGTDDKTR RSLLVTLVRIFCVRVIFAYDIRD GIHVRIIQINSKSGKVGSKHNSG YSAAKFGGVGLTQSLALDLAE YGITVHSLMLGNLLKSPMFQSL LPQYATKLGKIPDQVEQYYIDK VPFKRGCDYQDVNLMLLFYAS PKAVVLAPDSRSMSPAVSGRFG PRVVVAIALDDQQRIVDTL GLTVFARPKIPAITGRHSGATL QKQKCSVEELAQYFDTTGT MRKDLVILEHAGTVIRTSGGVV PDSPPHTRRDPRRFSMAFPWFD NIRSAEFHHVTLLAEIPRQOND IHRPAHAAAAPKVETRSGDET NRWNRPAQHLFA
30127	60495	A	30310	720	872	EKVPVSI GPGGMQELPMQSPDR RSAGKPGPASRAGR* TGGGAFS TKRDYR
30128	60496	A	30311	1967	2452	SRRCASINQRPRPGHEKMVS RIAPASNVPTCRPITVTTGSIALR SAWTIITRM RV SPLARAVRM* S SPSTSSIEERVIRTMTASGIVPST MAGKIIWATASIKLPSSPQMAV SISIKPVNGLESSRNTISLTRPET GVRFQCTETSMISIMPHQKIGIE
30129	60497	A	30312	1912	3960	
30130	60498	A	30313	2	250	LIRKVST*SVLMKAFLRIA*KDC ERLGLKCFWSGSEKGCPLVNT NAFGGHCEHHQWVSSVSRVRV SQSAGGCPLFNILLNTV
30131	60499	A	30314	1	300	SVFSH*AKKIWKGV SQRALGQ NSRSGSGCQASWTIRFPVGFH TDGTRLRRNPGMQAFLGPVAR FLALEARSLDCAFSSLLFKRKL SGRWGRASRGTKL

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30132	60500	A	30315	1	468	MTEKVKQQPAPVTASDEIDIGR LVGTVIEARWWVIGITTVFALC AVVYTFFATPIYSADALVQIEQ NSGNSLVQDIGSALANKPPASD AEIQLIRSRLVLGKTVDDLDDI AVSKNTFPIFGAGWDRMLMGRQ NETRRGFSARGTGQMLKKEGV TLMVEAIHASPGSEFTVTKYST LGMINQLHNSLTVTENGKDAG VLSLTYTGEDRYTNHAGVVNT MIIIAATHNLVFENNACEY AHP MGNAPAGLTEYQNVFYKH DRI QGHYVWEWRDHG IQAQDDHG NVWYKFGGDYGDYPNNYNFC LDGLIYSDQTPGPGLKEYKQVI APVKIHARDLTRGELKVENKL WFTTLDDYTLHAEVRAEGETL ATQQIKLRDVAPNSEAPLQITLP QLDAREAF LNITVTKDSRTRY S EAGHP IATYQFPLKENTAQPVP FAPNNARPLTLEDDRLSCTVRG YNFAITFSKMSGKPTSWQVNGE SLLTREPKINFFKPMIDN HKQEY EGLWQPNHLQIMQEHLRDFAV EQSDGEVLIISRTVKPRGP ARCP DSSVGTTYCTENNPPFDNGLLN AQLLQQA KPFVDERQSK*FGCH SPSYSCLWLSIIGLKKLIFGSRVS SDSPFTCQDVGLPLIFEKVI AKL
30133	60501	A	30316	1	524	
30134	60502	A	30317	1669	4421	
30135	60503	A	30318	2	349	SMAKCPLRKNQGPVRSCG AWS GCLWLPSPSGTPWRSSLWILL F/SQISQLLSLLHQGQFQPKPNH RGNKYLAKPGGSRSAIPD TDGP SARAGGQTDPEQE EGPLDPEED LSVKQLL
30136	60504	B	30319	217	368	
30137	60505	A	30320	1	951	
30138	60506	C	30321	1	3729	
30139	60507	A	30323	1	2437	

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30140	60508	A	30324	1005	1815	PDLHCQKKHPTLCSGYWPITFRT PVHYAAFS**/HALGHLAFS/EA SLHSHRGTQALTTQKKSPAKSP TAATTETRVMRKISHGTRDPPG FASLMQ*MHYGKLCFAFQSELL FQSLQRSHWTQSWWLCWPHW RLCWTQNNWWQCWPHWTLCW TQSWWLCWPHWRSCWTQRW WLCWPHWTLCWTQSWWLCW SHWRSCWTQSWWLCWPHWRI. CWTQSWWLCWPHWRSCWTQS WWLCWPHWRLCWSQSWWLC WPHWRLYWTQSWWLCWPHW RVCWTQN
30141	60509	A	30325	2436	3678	KMPWPWPSPGSPGLCSAWAEA PPAHCPCDVLHLHPACPHIQAP CGTGAPGTGLAAAADSEPLGSS APPAGRPCPQAAAACGLAPLP RGWCPPPTSSWMGRRLQSLSA HPTSPAPLLAAPTAVCSCSRCSA PRSRCVARPAARTGLPTPAPAS SPAPATSPAPAESPAATASHPV AEASPAPGAPPPRPAASPSAAS PAPPAASPVLTASPLPAASPAI. AASPVHTASPPVHVASPPVIITA SPPVHTASPPVHVASPPVHVAS PPVSCSGDSTSDCFPPQPGAVFP HSL/VSFLRWLVSSCSCSTLDGP AGGCGARGSAVWFLSLNKLLP/ MLLYQMYLMLLLLLRCANQ*I DVFSELTDYCGA*IQGYC*FLV LAIPR*VVTTTRSGCVRATAIDFL FPVSSCWNRALPLPICF
30142	60510	A	30326	929	2910	
30143	60511	A	30327	1	1488	
30144	60512	A	30328	203	701	
30145	60513	A	30329	493	924	SDPGFRHGKARITDPRGQPGRK LQGGSSSENGSMDKAARKVSG NKHSTSSHQHAVWC PGVPS*SG KAWAADQRFVPRILGKGRGHV DAA*LSWKCRNHLSSVSLNGE NQRFGVDARYRTRLQRGSANL FKRQRCGLHQNLELL
30146	60514	A	30330	1	2193	
30147	60515	A	30331	1	2990	
30148	60516	A	30332	2512	2560	FALRYRQPVRHRW*FHLVQRH GRFSRASGATWPASAAFAWP LLVCAPLSAASAAPLARL
30149	60517	A	30333	1	2820	
30150	60518	C	30334	194	418	
30151	60519	A	30335	25	458	



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30152	60520	A	30336	860	1209	IPGNCRDSSGVGIKERETNAGS QMHM/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAVPENPVYEKKPK KEVKKKRWNRSKMSLAQKKD WVAQKKASFLRA
30153	60521	A	30337	1	1440	
30154	60522	A	30338	138	512	
30155	60523	A	30339	1723	1845	
30156	60524	A	30340	6	983	RRWACRSLSSSGRRSLFRRMGF VKVVKNKAYFKRYQVKFRRRR EGKTDYYARKRLVIQDKNKYN TPKYRMIV\RVTNRDIIICQIAYA RIEGDMIVCATYAH\ELPKYGV KVGLTNYAAAYCTGLLLARRF L\NRFG\MDKIYEGQV\ELTGDE YNVESIDGQPGAFTCYLDAGLA RTTTGNKVFGALKGAVDGGLS YPLTPKRFPPWF/DDS*KPRNLI AEVHRKPHPWAQNVARLHAPT LMEED\EDA\YKKQFVRQYVKN SVT\PDMM\EEMY\KKAHAAIRE ESSSMEKKAQGGKFKKKRWNR P\KMSLAQKKDRVAQKKASFL RAQERGC
30157	60525	B	30341	1	2043	
30158	60526	A	30342	390	1180	
30159	60527	A	30343	2	649	
30160	60528	A	30344	1	1929	
30161	60529	A	30345	1	773	
30162	60530	A	30346	3	484	NSSCRDPGY/CPIIVSLNSS*GSL LQDMPGPSKVISEILATRGAVNI TTVAYKSAVILSFTTASAVSLSS RNVIGPLFASQPSFTIHFSLSHN GSAPLNAPDMANCFGLTALTSS LDERLFSRNSAGSCGIRNCFIS TLPPNTSTLTSVNSKGSSSVHG
30163	60531	B	30347	1	2775	
30164	60532	A	30348	1	1386	
30165	60533	A	30349	439	555	
30166	60534	A	30350	1	1785	
30167	60535	A	30351	100	488	IALASSHCTANARFRITRCRTK/ EQRYALSQAksiADELMTGCTN FAFSGKPGTGKNHLAALSGIAC WKTFLMNLASARDEKRAVVLH QIVDRRTASMRVGMILTNLNY EAMKTLLGERIMDRMTMNGG RW
30168	60536	A	30352	1	786	
30169	60537	A	30353	1	288	
30170	60538	A	30354	711	953	

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30171	60539	C	30355	1	2355	
30172	60540	A	30356	1035	1152	SPDSVDAQRGDADKPEL*GHE NIARRADYGSHDHERRAM
30173	60541	A	30357	1	420	
30174	60542	A	30358	1115	1561	
30175	60543	B	30359	501	555	
30176	60544	A	30360	441	602	SPPASWR**IPPAGFFT
30177	60545	A	30361	386	1647	
30178	60546	A	30362	1	1179	
30179	60547	A	30363	1	1215	
30180	60548	A	30364	1282	1657	
30181	60549	A	30365	388	804	
30182	60550	A	30366	1328	1978	
30183	60551	A	30367	455	1000	
30184	60552	A	30368	291	303	RVRRMMYTVTLYSFSTNKNTY I*E*E*G*GWRHHIFLG*MKCFS SRVILVLTSHDSSQSSLQTVSLL LLSSFALDPSSTMLTTEESVE
30185	60553	A	30369	284	433	RVRRMMYTVTLYSFSANKNTY I*E*E*GLGWRHHIFRGYM/RQH FND*SWP
30186	60554	A	30370	290	425	RVRRMMYTVTLSSFSANKNTYI *E*E*GLGWRHHIFLG*IQHFNR
30187	60555	A	30371	842	905	
30188	60556	A	30372	784	3453	
30189	60557	A	30373	1	209	
30190	60558	A	30374	36	412	ESEVLGPRSLPTWVPSGSLGP RGGRGGCILRPSRGGRGRHGPT KAGPWSPESRGR*DWKARGPP APSRGSPSRARARRGGSGGPA DEPGLQGRTRRPALSSRTSAPD PGRVVERSGRFRSES
30191	60559	A	30375	1	340	
30192	60560	A	30376	2	3336	
30193	60561	A	30377	22	419	
30194	60562	A	30378	1	13683	
30195	60563	A	30379	220	403	CLSTVFFLCITLVSECWSLF*SH MHVLLPRNRKEKLIEIFRTQTY DVNAYKASAHNRNSGPG
30196	60564	C	30380	169	415	
30197	60565	A	30381	3	1324	
30198	60566	A	30382	2	3455	
30199	60567	A	30383	85	2695	
30200	60568	A	30384	69	303	
30201	60569	A	30385	1	951	
30202	60570	A	30386	1	4749	
30203	60571	A	30387	176	1553	

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30204	60572	A	30388	1	425	MDQIISLFGRPDHVAYDIRSLRN KANPDDTFEAQLFYGDLKAIVK TSHLVKIDYPKFIVHGKKGFSIK YGIDQQETSLKANIMPGEFGFA ADDSVGVLEYVNDEGVTVREE MKPEMGDYG/PRL*CVVSNHHP RCAKLRQGI
30205	60573	A	30389	3	1890	PSQPLLWFAGRPRGRDTGCPRC KQNSTCIAAVKMEGPLSVFGDR STGETIRSQNDKESFNEQKTCRI *RKRLV*LYEVAEHEIVMAAAS IANIVKSSLGPGVGLDKML\VDDI GDVTITNDGATILKLLVEHPA AKVLCCELADLQDKEVGDTTS VVIIAAELLKNADELVKQEIHPT SVISGY\RLA\CKEAVRYINENP NLLTQDELGRDCLINAAKTSMS S\QIIGINGDFFANMVVDAVLAI KYTDIRGQPRYPVNSVNILKAH GRSQMESMLISGYALNCVVG QGMPKRIVNAKIACLDLQKT KMKLGVVQVITDPEKLDQIRQR ESDITKERIQKILATGANVILTT GGIDDMCLKYFVEAGAMAVRR VLKRDCLKRIAKASGATILSTLA NLEGEETFEAAMLGQA\EEVVQ ERICDDELILIKSTKA\RTSASIIS RVPIDSMCDEMERSL\HDALC\V VK\RVLESK\SVVPR\GGAVEAA LSIYLENYA\TSMGSREQLAIAR VCKITLWLPNTLSS*CLPRDST DLVLQNLRAF\HNEAQV\NPER\ KNLKWIGLDLSNGTTPRDNKQA GVFEPTIVKVRGLNFATEAAITN LRIDDLIKLHPESKDDKH/G/GS YEDAVHSGALND
30206	60574	B	30390	1	975	
30207	60575	B	30391	1	2577	
30208	60576	B	30392	1	3126	
30209	60577	B	30393	1	1134	
30210	60578	B	30394	1	2082	
30211	60579	B	30395	1	915	
30212	60580	B	30396	1	2658	
30213	60581	B	30397	1	2412	
30214	60582	B	30398	1	2454	
30215	60583	B	30399	89	2533	
30216	60584	B	30400	1	4083	
30217	60585	B	30401	1	1725	
30218	60586	C	30402	127	345	
30219	60587	A	30403	1	597	

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30220	60588	A	30404	3	3386	MPATASAGVPATVSEKQEFYQ LLKNI.INPSCMVRREQEEIYENI PGLCKTTFLDDAVRNRAGYE VRQMAAALLRRLSSGFEEVYP NLPADVQRDVKIELILAVKLET HASMRKKLCDIFAVLARNLID EDGTNHWPEGLKFLDISIYSTN VALWEVALHVFWHFGIFGTQ ERHDLDIKRLLDQCIQDQDHP AIKTL SARAAA FVL ANENNIA LFKDFADLLPGILQAVNDSCYQ DDDSVLESLEIADT
30221	60589	A	30405	1	1695	
30222	60590	A	30406	1126	1355	
30223	60591	A	30407	1	1610	MGSRCLNPPPPAHSDTTGKDSF GNIRGAETGQGASACSVTSARV TCGAGSEPHSHRNPGISAQVGL APSYGAARGRRRPLALQQSPQE RRHVGWNSTRGLLPASLPGTAS SQSASATASAALPLKVTGPLAR NPTPPWTA AAA LATRGQRPEK GLFPGPAPFSLGKRKRGRGRTW ERRRRVSIETSTCFRPGCERLGA AAGANLSQLASSQRPLRERWV LYTIIMAAAGAPDGMEEPGMD TEAETVATEAPARPVNCLEAEA AAGAAAEDSGAARGSLQPAPA QPPGDPAAQASVSNGEDAGGG AGRELVDLKIIWNKTKHDVKFP LDSTGSELKQKIHSITGLPPAMQ KVMYKGLVPEDKTLREIKVTS GAKIMVVGSTINDVLAVNTPK DAAQQDAKAEENKKEPLCRQK QHRKVLDKGKPEDVMPSVKGA QERLPTVPLSGMYNKS GGKVR LTFKLEQDQLWIGTKERTEKLP MGSIK\NVV\SDPI\EGHEDYHN DGRFQLAPTEA\SYWVYWVP TQYVDAIKD TVLGKWQYF
30224	60592	A	30408	71	415	WLFPPNPPVFRGQHPRQGLGPP SAAGR RAMKKKLVLCLLAVV LVLVIVGLCLW/LPSASKEPDN HVVTRATVAADAKQCSEIGRK\ AEVINAREVAPSVAFASMFNSS EQSQKAL
30225	60593	A	30409	562	2376	

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30226	60594	A	30410	604	2475	RQREVTRSPERSGLRVLQLFPP NPPVFRGQHPRQGLGPPSAAGR RAMKKKLVLVGLLAVVLVVI VGLCLWLPSASKEPDNHVYTR AAVAADAKQCSKIGRDALRDG GSAVDAAIAALLCVGLMNAHS MGIGGGLFLTINYNSTTRKAEVIN AREVAPRLAFATMFNSSEQSQK GGLSVAVPGEIEGYELAHQRHG RLPWARLFQPSIQLARQGFPVG KGLAAALENKRTVIEQQPVLCE VFCRDRKVLREGERLTLPQLAD TYETLAIEGAQAFYNGSLTAQI VKDIQAAGGIVTAEDLNMYRA ELIEHPLNISLGDAVLYMPSAPL SGPVLALILNILKGYNFSRESVE SPEQKGLTYHRIVEAFRFAYAK RTLLGDPKFVDVTEASSGVSA\ VVRNMTSEFFAAQLRAQISDDT THPISYYKPEFYTPDDGGTAHL SVVAEDGSAVSATSTINLYFGS KVRSPVSGILFNNEMDDFSSPSI TNEFGVPPSPANFIQPGKQPLSS MCPTIMVGQDGQVRMVVGAA GGTQITTATALAIYNLWFGYD VKRAVEEPRLHNQLLPNVTTVE RNIDQAVTAALETRHHHTQIAS TFIAVVQAIVRTAGGWAAASDS RKGGEPAHY
30227	60595	A	30411	63	342	GRTLPHGGLPHHYLVQCEWL PGTS*AEFPVVHLPAFVARARG ADRQHHGPFLPLCHLHPARPRR EDLHRKSPGEPNPIEHHRSSGPG CRRI
30228	60596	A	30412	1	910	MLFRPALGSRQVVRNMTSEFF AAQLRAQISDDTTHPISYYKPEF YTPVDGGTAHLSVVAEDGSAV STTSTINLYFGSKVRSPVSEILFN DEMDDFSSPNITNEFGVPPSPAN FIQPGMGWRKQPLSSMCPTIM VGQDGQVRMVVGAAAGGTQITT ATALICVTAFLPGRAHPAQPPS HADHTPMPQAIYNLWFGYDV KRAVEEPRLHNQLLPNVTTVER NIDQAVTAALETRHHHTQIAST FIAVVQAIVHTAGGWAAASDS RKGGAIRLSALQEDKADKQS RDKILTRTRKGLGDWLPM

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30229	60597	A	30413	110	868	DLCPLPTLPPHLLRPALGSRQV VRNMTSEFFSAQLRAQISDDTT HPISYYKPEFYMPDDGGTAHLS VVAEDGSAVSATSTINLYFGSK VRSPVSGILLNNEMDDFSSTSIT NE\LGVPSPANFIQPGKQPLSS MCPTIMVGQDGQVRMVVGAA GGTQITMATALAIYQPSWFGY DVKRAVEEPRLHNQL\LPNVT VERNIDQAVTAAL\ETRHHTQ IASTFI\AVVQAIVRTAGGWAAA SDSRKGGEPAGY
30230	60598	A	30414	1	1626	
30231	60599	A	30415	171	2097	PSGEREGCLIRESLKKILWLQAS AECEGDPGYFLSYFHQILLSFV ANTPRQGLGPPSAAGRRAMKK KLVVLGLLAVVLELVIVGLCL WLPSASKEPDNHVYTRAAVAA DAN\CSKIGRDALRDGGSADV AAIAALLCVGLMNAHSMGIGG GLFLTINSTTRK\AEVINAREV APRLAFATMFNSSEQSQKGGLS VAVPGEIRG\YELAHQRHGRLP WARLFQPSIQLARQGFVPGKGL AAALENKRTVIEQQPVLCEVFC RDRKVLREGERLTLPQLADTYE TLAIEGAQAFYNGSLTAQIVKDI QAAGGIVTAEDLNNYRAELIEH PLNISLGDAVLYMPSAPLSGPV LALILNILKGYNFSRESVESPEQ KGLTYHRI\VEVFRFAYAKRTL LGDPKFVDVTEASSGVSA\VVR NMTSEFFAAQLRAQISDDTTHPI SYYKPEFYTPDDGGTAHLSV AEDGSAVSATS\ITINLYFGSKVR SPVSG\ILFNNEMGDLSSPSITN EFGAPSPANFIQPGKQPLSMC LTIMVGQDGQVRMVVGAAAGG TQITTDALAIIN\LCFGYDVK RAVEEPRLHNKLLPNVTVERN IDQAVTAAL\ETRHHTQIASTFI AVVQAIVRTAGGWAAASDSRK

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30232	60600	A	30416	645	2571	GRPRLFPQLFPPNPPVFRGQHPR QGLGPPSAAGRRAMKKKLVL GLLAVVLVLVIVGLCLWLPSAS KEPDNHVYTRAAVAADAKQC SEIGRVLVGGPAYLLLLGKAEV INAREVAPRLAFASMFNSSEQS QKGGLSVAVPGEIRGYELAHQ RHGRLPWARLFQPSIQLARQGF PVGKGLAAVLENKRTVIEQQPV LWYVCGKVLREGERLTLPLRA DTYEMLAIEGAQAFYNGSLMA QIVKDIQAAGGIVTAEDLNMYR AELIEHPLNISLGDAVLYMPSA RLSGPVLALILNILKGYNFSRES VETPEQKGLTYHRIVEAFRFAY AKRTL LGDPKFVDVTENSIAGL LCARMDSPALGSRQVVRNMTS EFFAAQLRSQISDHTTHPISYYK PEFYTPDDGGTAHLSVVAEDGS AVSATSTINLYFGSKVCSPVSGI LFNNEMDDFSS\PAFTNEFGAPP SPANFIQPGKQPLLSMCLTIMV GQDGQVRMVVGAAGGTQITTD TALPPSHADHTPMPQAIHYNLW FGYDVKRAVEEPRLHNKLLPN VTTVERNIDQAVTAALETRHH HTQIASTFIAVVQAIVRTAGGW AAALDSRKVPTPGAGFWGLV EVGWWEAVITAQHLDITRGTG
30233	60601	A	30417	5	439	
30234	60602	A	30418	1	423	

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30235	60603	A	30419	97	2012	WADEETWLCLPHLPVFSPTAHL PLLSSTPFSSLLPFISTPHPRGFA LPLPPSARLYLELRKLPATLPWS SVTDTGSYLSGRRERGEGEGP GRRVRVADHGFALPRTGPQGS EEELANMQGL\VERLERAVSRL ES\SAESHRPPGN\CGEVNGVI A\GVAPSRGKPLHKLMDSMVA EF\LKNSRILSGDVETLAEIVHS AFQAQRAFLLMASQYQQPHEN DV\AALLKP\ISEK\KEIQTFQRE /RTRGSNMFNHLSAVSE*IPCPL DGI\AVSPKPG\PY\VKEMND\AA TFYTNRVLKD*KQSDLRHVDW VKS\YLN\WSELQAYIKEHHTTG LTWE\SKTGPV\ASTVS\AFSVLS SGAWGFPPPPPLPPPG\PPSTFS EEWKGKKEESSPSR\SALFAQL N/QGEKAITKGLRHVTDDQKT YKNPSLRAQGGQTQSPTKSHTP SPTSPKSYPSQKHAPVLELEGK KWRVEYQEDRIDLVISETELKQ VAYIFKCEKSTIQIKGKVNSIID NCKKLGLVFDNVVGIVEVINSQ DIQIQVMG\RVPTIS\NKTEGCH IYLS\EDALDCE\VS\AKSIWKWN ILYPPQGWVD\YREFPHF\PEQF KTS/AWDGS\KLITE\AEIMALT SLRDRTSPESPSPSIKTNKKA\VK
30236	60604	B	30420	1	499	
30237	60605	B	30421	390	851	
30238	60606	B	30422	136	603	
30239	60607	B	30423	1	2190	
30240	60608	A	30424	82	242	
30241	60609	A	30425	1	330	



SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30242	60610	A	30426	215	1984	LLLVV TMSNNGLDIQDKPPAPP MRNTSTMIGAGSKDAGTLNHIG SKPLPPNPEEKKKKDRFYRSILP GDKTNKKKEKERPEISLPSDFE HTIHVGFDVAVTGEFTGMPEQW ARLLQTSNITKSEQKKNPQAVL DVLEFYNSKKTSNSQKYMSFTS GDKSAHG YIAAHPSSTKTASEP PLAPPVSEEEDEEEEEEDENEP PPVIAPRPEHTKSIYTRSVVESIA SPAVPNKEVTPPSAENANSSTL YRNTDRQRKKSKMTDEEILEKL RSIVSVGDPKKKYTRFEKIGQG P\SGTVYTAMDVA TGQEVAIKQ MNLQQQPKKELIINEILVMREN KNPNI VNYLDSYLVGDELWVV MEYLAGGSLTDVVTETCMDEG QIAAVCRECLQALEFLHSNQVI HRDIKSD\NILLGMDGSVKI.TDF GFCAQITPEQSKLSTHG*GTPY W\MAPEVVDTERAYGPK/VLDI W\SLGIMAIEMIEGEPYLNENP LRALYLIATNGTPELQNPEKLAS AIFR\DFL\NRCLEMDVEKRGFS/ SKELLQHQLKIGQAPSPSLTPH *LLQPKEATKEQSPKTHTHPQP HCAQAFCEINAHFRNSNS
30243	60611	A	30427	2	337	
30244	60612	A	30428	1	1644	
30245	60613	A	30429	1	330	
30246	60614	A	30430	169	440	
30247	60615	A	30431	1	1689	
30248	60616	A	30432	17	283	GHAWQLASIWLLCLLWPAVPL NCLSSYGWTLWWRIALVGA*R SLAPSRGSWSTQARPLKQRRTK WCGKSWCLSGTSEPLSHWPRI. RSW
30249	60617	A	30433	16	346	RTDTYHLEDSKEQSGNRAGSG GWL*SCAE/GRRVALKSWPGRT GMSGTRRV TASSRGTSWYCGG SAGRSSTPPTGRACSPGFSFSP PQPPGPSAAGSSVSGQLGPCGG
30250	60618	A	30434	1	1772	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30251	60619	A	30436	1	2607	MLTMSVTLSPLRSQDLDPMAT DASPMANMTPTVEQGEGER MKDMDSQDQYKPPPLHTGAD WKIVLHLPEIETWLRMTSERVR DLTYSVQQSDSKHVDVHLVQ LKDICEDISDHVEQIHALLETF SLKLLSYSVNVIVDIHAVQLLW HQLRVSVLVLRERILQGLQDAN GNYTRQTDILQAFSEETKEGRL DSLTEVDDSGQLTIKCSQNYLS LDCGITAFELSDYSPSEDLLSGL GDMTSSQVKTKPFDSWSYSEM EKEFPPELIRSVGLLTVAAADSIST NGSEAVTEEVSVQSVLSVDDKG GCEEDNASAVEEQPGLTLGVSS SSGEALTNAAPPSSETVQQESS SSSHHDAKNQQPVPENATPKR TIRDCFNYNEDSPTQPTLPKRGL FLKEETFKNDLKGNGGKRQMV DLKPEMSRSTPSLVDPDRSKL CLVLQSSYPNPSAASQSYECL HKVGNGNLENTVKFHIKEISS LGRLNDCYKEKSRLKKPHKTSE EVPPCRTPKRGTGSGKQAKNT KSSAVPNGELSYTСКАIEGPQT NSASTSSLEPCNQRSWNAKLQL QSETSSSPAFTQSSSESVGSDNI MSPVPLLSKHKSKKGQASSPSH VTRNGEVVEAWYGSDEYLALP SHLKQTEVLALKLENLTCLLPQ KPRGETIQNIDDWELSEMNSDS EIYPTYHVKKKHTRLGRVSPSS
30252	60620	A	30437	1	1983	
30253	60621	B	30438	1	702	
30254	60622	B	30439	1	936	
30255	60623	B	30440	1	1494	
30256	60624	B	30441	1	921	
30257	60625	B	30442	1	3342	
30258	60626	B	30443	1	1072	
30259	60627	B	30444	1	3711	
30260	60628	B	30445	15	674	
30261	60629	B	30446	1	2127	
30262	60630	B	30447	1	3132	
30263	60631	B	30448	103	438	
30264	60632	B	30449	1	3042	
30265	60633	B	30450	1	1425	
30266	60634	B	30451	84	1954	
30267	60635	B	30452	1	1419	
30268	60636	B	30453	130	1615	
30269	60637	B	30454	1	1794	
30270	60638	B	30455	1	3255	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30271	60639	B	30456	1	945	
30272	60640	B	30457	1	7437	
30273	60641	B	30458	1	1122	
30274	60642	B	30459	317	1630	
30275	60643	B	30460	1	1716	
30276	60644	B	30461	46	915	
30277	60645	B	30462	1	624	
30278	60646	B	30463	244	2988	
30279	60647	B	30464	1	804	
30280	60648	B	30465	1	1455	
30281	60649	B	30466	1	732	
30282	60650	B	30467	340	777	
30283	60651	B	30468	1	714	
30284	60652	B	30469	166	1337	
30285	60653	B	30470	72	617	
30286	60654	B	30471	1	1002	
30287	60655	B	30472	1	4173	
30288	60656	B	30473	1	4488	
30289	60657	B	30474	1	3822	
30290	60658	B	30475	1	1866	
30291	60659	B	30476	1	1002	
30292	60660	B	30477	1	1407	
30293	60661	B	30478	99	1046	
30294	60662	B	30479	122	1113	
30295	60663	B	30480	302	4145	
30296	60664	B	30481	1	669	
30297	60665	B	30482	1	933	
30298	60666	B	30483	1	2136	
30299	60667	B	30484	1	4017	
30300	60668	B	30485	1	1335	
30301	60669	B	30486	1	1095	
30302	60670	B	30487	1	2895	
30303	60671	B	30488	1	1215	
30304	60672	B	30489	1	2001	
30305	60673	B	30490	1	1281	
30306	60674	B	30491	1	780	
30307	60675	B	30492	1	858	
30308	60676	B	30493	1	699	
30309	60677	B	30494	1	1624	
30310	60678	B	30495	1	2958	
30311	60679	B	30496	30	658	
30312	60680	B	30497	1	1755	
30313	60681	B	30498	1	631	
30314	60682	B	30499	1	1528	
30315	60683	B	30500	1	1056	
30316	60684	B	30501	1	2305	
30317	60685	B	30502	1	723	
30318	60686	B	30503	1	2691	
30319	60687	B	30504	1	2322	
30320	60688	B	30505	401	2677	
30321	60689	B	30506	1	1218	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30322	60690	B	30507	1	906	
30323	60691	B	30508	1	2865	
30324	60692	B	30509	45	820	
30325	60693	B	30510	1	783	
30326	60694	C	30511	18	410	
30327	60695	B	30512	1	840	
30328	60696	B	30513	1	945	
30329	60697	B	30514	1	2108	
30330	60698	B	30515	1	2457	
30331	60699	B	30516	1	1156	
30332	60700	B	30517	43	4677	
30333	60701	B	30518	80	964	
30334	60702	B	30519	1	4521	
30335	60703	B	30520	1	2460	
30336	60704	B	30521	1	1854	
30337	60705	B	30522	1	1367	
30338	60706	B	30523	273	419	
30339	60707	B	30524	1	1786	
30340	60708	B	30525	1169	1443	
30341	60709	B	30526	1	486	
30342	60710	B	30527	13	1260	
30343	60711	B	30528	270	723	
30344	60712	B	30529	1	834	
30345	60713	B	30530	1	1632	
30346	60714	B	30531	1	4831	
30347	60715	B	30532	184	1593	
30348	60716	B	30533	1	615	
30349	60717	B	30534	1	3513	
30350	60718	B	30535	113	1666	
30351	60719	B	30536	101	2667	
30352	60720	B	30537	1	1692	
30353	60721	B	30538	51	142	
30354	60722	B	30539	1	3198	
30355	60723	B	30540	251	1207	
30356	60724	B	30541	1	1491	
30357	60725	B	30542	1	4024	
30358	60726	B	30543	1	3316	
30359	60727	B	30544	1	1342	
30360	60728	B	30545	91	810	
30361	60729	B	30546	17	489	
30362	60730	A	30547	1	504	MGGSNRS AEAWKLANGINIIVA TSGRLLDHMQNTPGFMYKNLQ CLVIDEADRILDVGFEEELKQII KLLLTHRQTMLFSATQTQKVE DLARISLKKEP/LYVGDDDDNA NETVFGTLLCTDVAARGLDITE VDCIVQYDPPDDPKEYIHSVGR TARGLNGRENWVFFAT
30363	60731	A	30548	1	2676	
30364	60732	B	30549	1	1071	
30365	60733	A	30550	1	348	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30366	60734	A	30551	1	711	MAEIQHK TIRPLLEGRDLLAAV KTGSGKTLAVLIPAIELVVKLKF MPRNGTGVLILSPTRQLAMQTF GVLKELMTHHVHTYGLIIGGSN RSAEAQKLANGINIIVVTPGRLL DHTQNTPGFMYKNLQVEDLAR ISPKKEPLYVGVDEDKANATVD GLEQGHFVCPSEKRYLLLF TFL KKNQKKKLMVFFSACMSVKYP YGLLYIDL/PVLAIHGKQKQN KHTTTFF*YCNADSGTLL
30367	60735	A	30552	661	987	VTFYSSEHSNPCHKNLRKARRK DTKRIILKW*HTLV*GRDI*N*NI IITRNTRYSLLCPWATKKLKAC FISQK*KRDVIERN SAQCLQPKS IYTLVR*VQILKSTKILL
30368	60736	A	30553	188	2188	KFQGASNLTLSETQNGDVSEET MGSRKVKKSKQKPMNVGLSET QNGGMSQEAVGNIVTKSPQK STVLTNGEAA MQSSNESK GK MKKKRKMVND AEPDTKKAKT ENKGKSEEE SAETT KETENNVE KPDNDEDESEVPSLPLGLTGAF EDTSFASLCNLVNENTLKAIKE MGFTNMTEIQHKSIRPLLEGRD LLAAAKTGSGKTLAFLIPAVELI VKLRFMPRNGTGVLILSP TRE LAMQTFGVLKELMTHHVHTY G LIMGGSNRS AEAQKLGNGINIIV ATPGRLLDHMQNTPGFMYKNL QCLVIDEADRILDVGFEEELKQI IKLLPTRRQTM LFSATQTRKVE DLARISLKKEPLYVGVDDDKA NATVDGLEQGYV\VCPSKRFL LLFTFLKKNRKKLMVFFSSCM SVKYHYELLYIDL PVLAIHGK QKQNKRT\TFFQFCNADSG\TL LCT\DV\AARGLDIPEVDWIVQY DPPDDPKEYIHRVG*EQPEGLN GEEGHALASFLRPRKDLGFFFR LL*KHSGGFPLSGIWTF SW/SLK ISDIQFSAWRNWIGKVITFLHKS A\QEAYKSYITEPMDSPFL*NRS FN\VN NLN LASGLLCQGF K\VP PFVDLNVNSNEGKQKKRGGGG GFG LPRKTQEKLEKS\KIF*TH* ARKSSGQAGQFSH

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively  
25 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - 30 (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-30368.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- 5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample under stringent hybridization conditions with
- 10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the
- 15 sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is
- 25 detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-30368, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 30369-60736, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-30368.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.



27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

- 5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 15/00, 15/12

US CL : 536/23.1, 23.5; 435/6, 320.1, 325

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 23.5; 435/6, 320.1, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched  
NONEElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
NONE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P --- A	Database Genbank, Accession No. AL135937, 15 March 2001 (15.03.2001), particularly nucleotides 29925 through 30325.	1-8 ----- 9, 19
X --- A	Database Genbank, Accession No. AA004350, HILLIER et al., Generation and analysis of 280,000 Human Expressed Sequence Tags. Genome Res. 07 May 1997 (07.05.1997), Vol. 6, No. 9, pages 807-828.	1-8 ----- 9, 19

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

\* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&amp;"

document member of the same patent family

Date of the actual completion of the international search

23 October 2001 (23.10.2001)

Date of mailing of the international search report

02 JAN 2002

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

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Form PCT/ISA/210 (second sheet) (July 1998)

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1

Remark on Protest

☐  
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-9 and 19, drawn to polynucleotides.

Group II, claim(s) 10-11, drawn to polypeptides.

Group III, claim(s) 12, drawn to antibodies.

Group IV, claim(s) 13-15, drawn to methods of detecting polynucleotides.

Group V, claim(s) 16, drawn to methods of detecting polypeptides.

Group VI, claim(s) 17, drawn to a first method of identifying compounds that bind.

Group VII, claim(s) 18, drawn to a second method of identifying compounds that bind.

Group VIII, claim(s) 20-21, drawn to polypeptide arrays.

Group IX, claim(s) 22-26, drawn to polynucleotide arrays.

Group X, claim(s) 27, drawn to a method of treatment using a polypeptide.

Group XI, claim(s) 28, drawn to a method of treatment using an antibody.

In addition, each of the SEQ ID NOS. named in the groups is considered to be a separate invention and applicant must elect a single SEQ ID NO. or for Groups VIII and IX a specific combination of SEQ ID NOS. for searching. Due to the burden of search for sequences, only a single SEQ ID NO. or specific combination of SEQ ID NOS. for Groups VIII and IX is considered to meet unity of invention.

The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the products of Groups I, III, VIII, and IX differ structurally and functionally and thus lack the same or corresponding special technical feature. Each of the methods of Groups IV-VII, X and XI have different starting materials, method steps, and goals and thus lack the same or corresponding special technical feature.

As each SEQ ID NO. does not appear to share a common core structure, they are considered to be structurally and functionally distinct invention.

The number of inventions has been determined as follows: Each of groups I-XI is directed to 30368 SEQ ID NOS. As such, 30368 SEQ ID NOS. X 11 groups results in 334048 inventions.

If no additional fees are paid, Group I, claims 1-9 and 19, will be searched with respect to SEQ ID NO: 1. If Group VIII is elected, the default polypeptide array is considered to be an array comprising all of SEQ ID NOS: 30369-60736. If Group IX is elected, the default polynucleotide array is considered to be an array comprising all of SEQ ID NOS: 1-30368. Applicant is advised that they should specifically identify each additional group and each additional SEQ ID NO. being paid for. With respect to Groups VIII and IX, applicant should specifically identify each subset of SEQ ID NOS. present on the arrays if additional combinations are to be searched.